

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGCTCGGGCTAGTC**ATG**GCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTCAGAGACGTTCTGCTAATCTACACTTTATTTTC
TGGATCACTGGCGTTATCCTTCTGCAGTGGCATTTGGGCAAGGTGAGCCTGGAGAATTA
CTTTCTCTTTAAATGAGAAGGCCACCAATGTCCCCTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTGGCACCTTGGTTGTTGCTACCTGCCAGCTCTGCATGGATGCTA
AAACTGTATGCAATGTTCTGACTCTCGTTTTGGTCGAAGTGGCGCTGCCATCGTAGG
ATTGTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTGAAGC
AGTATAACTCTACAGGAGATTATAGAACGCATGCAGTAGACAAGATCCAAAATCGTTGCAT
TGGTGTGGTGTACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAACCTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTCCTTGGAGTTGCTTGCCTCAACTGATTGGAATCTTCTGCCACTGCCWCTCTCG
TGCCATAACAAATAACCACTGAGATAGTGT**TAA**CCCAATGTATCTGTGGCCTATTCTCT
CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTGATAGACCAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGCTGAT
TCAATCAAGATGTATGTTGCTATGTTCAAGTCCACCTCTATCCCATTCAATGTTAGATCG
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
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VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCCTGCCACCCGGGGCGTGGGAGTGAGGTACCAATTAGCCCATTGGCC
CCGACGCCTCTGTTCTCGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTAACGGACTG
CAAGATGGAGGAAGGCAGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTCGTCTCAGGCTTCCTGCTTTCCGAAGC
CTTCCCCGACATACTTCGGACTAGTGCAGAGCAAACCTTTCCCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTGGCTTACAGCATGCTGGCTCAGCTCA
CATTCTGGGAGGCCAGCAGCTTACCTGCTGTTGAGCCTACGCTGGCCACTGTCAAC
GCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTCTTCCGCTACCATGGGCTGTCC
TCTCTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCGCTGGCCTGCCCTGGA
AATAAGGAGCCTTAGCATGGGCCCTGCATGCTAATAATGCTTCTCAGAAATGAAAAAAA
AAAAAAAAAAAA

FIGURE 6

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<subunit 1 of 1, 231 aa, 1 stop
<NX(S/T): 0
MEEGGNLGGGLIKMVHLLVLSGAWGMQMWMVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLLATVNARWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTAAAGCCCATTCTGCAGTGGAAATTCTGAACTAGCAAGAGGAACCCATCTT
 CTTGTATTATAACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTGGGT
 GCTAGGCCTCCTAATCCTCTGGTTCTGGACTCGTAAAGGAAAACAAAGATTGAAG
 ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCC
 AGAACCTTGATAAAAAGGGATTCATGTAATCGCTGCCGTCTGACTGAATCAGGATCAAC
 AGCTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGAATGCCAGTGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGT
 CTGATCAATAATGCTGGTGTCCCCGGCGTGGCTCCACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGGAGGTCGCCCTGCA
 ATCGTTGGAGGGGGCTATACTCCATCAAATATGCAGTGGAAAGGTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
 ACTTGGCAGATCCAGTAAAGGTAAATTGAAAAAAACTGCCATTGGGAGCAGCTGTCTCCA
 GACATCAAACAACAAATGGAGAAGGTTACATTGAAAAAAAGTCTAGACAAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCCGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTCCCTAAGACTCATTATGCCCTGGAAAAGATGCCAAATTCTGGATACCTCTG
 TCTCACATGCCAGCAGCTTGAAGACTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGTGTGACTCAGCTAACCAAAATGTCTCCAGGCTATGAAATTGGCGAT
 TTCAAGAACACATCTCCTTCAACCCATTCTTATCTGCTCCAACCTGGACTCATTAGA
 TCGTGCTTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTAGGTACATCACA
 ATAGGCAAGTCCTGCCCTGT
 ATTAGGCTTGCCTGCTGGTAGTGAAGGGAAATTGAAAGACTTGCCCATTCAAATG
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 AAAAAAAAAAAAAAA

FIGURE 8

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LTLEDYREPPIEVNLFGLISVTLNMLPLVKKAQGRVINSSVGGLAIVGGGYTPSKYAVEGF
NDSSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSIFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GC GGGCTGTTGACGGCGCTGCG**ATGG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTCCTGACGCCGAGTGGCGGGCCCTGGGCGCTGCCACCACT
 GTAGTCATGTACCCACCGCCGCCGCGCTCATCGGGACTTCATCTCGGTGACGCTGAG
 CTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGCGCTCGTGTGGAGGAATGGA
 AGCAACTGTCGAGATTGACAGCGGAATATGATTCTCTCCTGCCTTGCTTTCTGCTTTCTGT
 GGACTCCTCTTACATCAACTGGCTGACCATTGAAAGCTCTGGCTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGTTAAAACCAGCAAATCCACCCGTCTTACCA
 CTCCTCAGAAGGCAGCACCGACCCCTGAGAACATTACCTGAGATTGTCACAGAAAGACCAA
 AGACACATCCAGCGGGGACACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA
 TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGGCCCTGTGGATCCCCGCCGAAGGAG
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 CTCCCTCAAGAAGAGCAGAAGTGCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG
 CACACCAGTGCATCTGAACATCGCCAGAAGGGCGTGATTGACGCTTCTGCATGCATGGA
 AAGGATAACCGCAAGTTGCATGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTCAGT
 GAGTGGTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTGGGTCT
 GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTGAAAAGGACG
 TGGACGTCAACCTGTTGAGAGCACGATCCGCATCCTGGGGGGCTCTGAGTGCCTTACAC
 CTGTCTGGGGACAGCCTCTCCTGAGGAAAGCTGAGGATTTGAAATCGGCTAATGCCTGC
 CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTTACTGGAGTTGCCACC
 CGCCACGGTGGACCTCGACAGCACTGTGGCGAGGTGACCAGCATTAGCTGGAGTTCCGG
 GAGCTCTCCGTCTCACAGGGATAAGAAGTTCAAGGAGGCAGTGGAGAAGGTGACACAGCA
 CATCCACGGCCTGTCTGGGAAGAAGGATGGCTGGTGCCTATGTTCAATACCCACAGTG
 GCCTCTCACCCACCTGGCGTATTACAGCTGGCGCCAGGGCCAGCAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGAAGCAGGAGACACAGCTGCTGGAAAGACTACGTGGA
 AGCCATCGAGGGTGTCAAGACGCACCTGCTGCGGCACTCCGAGCCCAGTAAGCTCACCTTG
 TGGGGGAGCTTGCCTACCGGCCCTCAGTGCCTGGCAAGATGGACCACTGGTGTGCTTCTGCCA
 GGGACGCTGGCTCTGGCGTCTACCACGGCCTGCCAGCCACATGGAGCTGGCCAGGAGA
 GCTCATGGAGACTTGTACCAAGATGAACCGGAGATGGAGACGGGCTGAGTCCCAGATCG
 TGCACTTCAACCTTACCCCCAGCCGGCGTCGGGACGTGGAGGGTCAAGCCAGCAGACAGG
 CACAACCTGCTGCGGCCAGAGACCCTGGAGAGCCTGTTACCTGTACCGCGTCACAGGGGA
 CCGCAAATACCAGGACTGGGGCTGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCC
 CCTCGGGTGGCTATTCTCCATCAACAAATGTCCAGGATCCTCAGAAGCCCGAGCCTAGGGAC
 AAGATGGAGAGCTTCTCTGGGGAGACGCTCAAGTATCTGTTCTGCTTCTCCGATGA
 CCCAAACCTGCTCAGCCTGGACGCCACGTGTTAACACCGAAGCCCACCTCTGCTATCT
 GGACCCCTGCC**TAGGGTGGATGGCTGCTGGTGTGGGACTTCGGGTGGCAGAGGCACCTG**
 CTGGGTCTGTGGATTTCAGGGCCACGTAGCACCGCAACCGCCAAGTGGCCAGGGCT
 CTGAACCTGGCTCTGGCTCCTCGTCTGCTTAAATCAGGACACCGTGAGGACAAGTGA
 GCCCGTAGCTTGGTGTGATGCCGGGTGGCTGGGCCCTGGAGCCTCCGCTGCTTCTC
 CAGAACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA
 GAGGGGGCTCGAGGTGGTCCCTGGTACTGGGTGACCGAGTGGACAGCCCAGGGTGCAGC
 TCTGCCGGCTCGTAAGCCTCAGATGTCCCCAATCCAAGGGCTGGAGGGCTGCCGTGA
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTGGTGTAAAGCTGGACTCAGGGATCCTC
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 CCAGTGGAATGGGTCTTCTGGAGATAAAAGTTGATTGCTCTAACCGCAA

FIGURE 10

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
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><MW: 79553, pI: 7.83, NX(S/T): 0
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IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPLPPARTQGTPVHLNY
RQKVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTLGVFTL GARADSYYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNL RPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA

```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCGGAGGCCGGCCGGCTGCAGGCCCTGCCCATGCGCCGC
 CGCCTCTCCGCACG**ATG**TTCCCCTCGCGAGGAAAGCGGCCAGCTGCCCTGGGAGGACGGC
 AGGTCCGGGTTGCTCTCCGGCCCTCCCTCGGAAGTGTCCGTCTCACCTGTTCGTGGC
 CTGCCTCTCGCTGGGCTTCTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGACGTGG
 CCCGGGCAGTCAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCCAGAG
 CCGCCCCCTGAGCACTGGAAAGAACGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
 GCCCTCCGCGAACGCTTCGAGGAGCTCCTGGTCTCGTGCACATGCGCCGCTCCTGA
 GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACCTCAGGTTAAC
 CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGAACAGCACGGACTACATTGCCAT
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTCCTGAGGCTGGC
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCCTCTACCAACTACAAGACCTATGTCGGCGGC
 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTCAATGGATGTCCAACCGCTCTGGGG
 CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGATTAAGGGAGCTGGCTCCAGCTTTCC
 GCCCTCGGAATACAACACTGGGTACAAGACATTGCCACCTGCATGACCCAGCCTGGCGG
 AAGAGGGACCAGAACGCGATCGCAGCTAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
 AGGCCTGAACACTGTGAAGTACCATGTGGCTCCCGACTGCCCTGTCTGTGGCGGGGCC
 CCTGCACTGTCCTAACATCATGTTGGACTGTGACAAGACGCCACACCCCTGGTGCACATT
 AGC**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATTGCTCAGGCTCAGGA
 CAAGGCCTCAGGTCGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
 AGCTACGCAATTGCAGCCACCCGGCCAAAGGCAGGCTGGCTGGCCAGGACACGTGGG
 GTGCCCTGGGACGCTGCTGCCATGCACAGTGATCAGAGAGAGGCTGGGTGTCCCTGTCCG
 GGACCCCCCCTGCCTCCTGCTCACCTACTCTGACCTCCTCACGTGCCAGGCCTGTGGG
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FIGURE 12

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><subunit 1 of 1, 327 aa, 1 stop
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MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR
GQQQETSGPPRACPPEPPPHEWEEDASWGPRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHIIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDV DLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILL SKQHYRLCNGMSNR FWG WGREDDEFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIA A QKQE QFKV DREGGLNTVKYHV ASRTA LSVGGAPCTVL
NIMLD CDTAT PWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTGCCTATCCACCTCCCCAAGCCCCTTACCTATGCTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTAAAGGCTCATGCTTGGAGTGGGACTGGTCGGTGCCCAGAAAGTCT
CTTCTGCCACTGACCCCCATCAGGGATTGGCCTTCTTCCCCCTCCTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT
GGGGGATGGCTAAGAAAGCTGGAGATAGGAACAGAAGAGGGTAGTGGGTGGCTAGGGGG
GCTGCCTTATTAAAGTGGTTATGATTCTTATACTAATTATAACAAAGATATTAAGGC
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FIGURE 14

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PRGEGEKVGDG
```

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGAACAAAG
 GAGCATGTCCCGCCGGGAAGGCCGTCCTCCGGCCGCATAAGGCTCCGGTCGCCGCTGG
 GCCCGCGCCCGCGCTCTGCCGCCGGCTCCGGGGCGCCGCTAGGCCAGTGCGCCGCG
 CTCGCCCCGCAGGCCCGGCCGCAGC**ATG**GAGCCACCCGGACGCCGGCGGGCGCGCA
 GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTCGCGCTGCTGGGAGGCGGCG
 GCAGGCCGGCGCCGCCGGCGCTGCCGCCGGCTGCAAGCACGATGGCCGGCCCGAGGGGCTGG
 AGGGCGGCCGGCGCCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACTCGGCAGGTCT
 GCCCCCAGATACTCTGCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCG
 AGCTGAAGAATGGCTCATTCTGGGTTAAGTCTCCTGAAAGATTGGACCTCCGAAACAAT
 CTTATTAGTAGTATAGATCCAGGTGCCTCTGGGACTGTCATCTCTAAAAAGATTGGATCT
 GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTCGAGGACTCACCAATCTGGTTC
 GGCTAAACCTTCGGGAAATTGTTCTCATTATCTCAAGGAACCTTGTATTCTTGCG
 TCATTACGGTCTTGGAAATTCCAGACTGAGTATCTTTGTGTGACTGTAACATACTGTGGAT
 GCATCGCTGGTAAAGGAGAAGAACATCACGGTACGGGATACCAAGGTGTGTTATCCTAAGT
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 GAATTGCCGTCTTCTACATGACTCCATCTCATGCCAAGTTGTGTTGAAGGAGACAGCCT
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 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTGTTGAAAAGAACATGATTCAAAC
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 GACATTGCAAGTAACATCATGTTGGCTGATGAAACGTGTCCTGTGGCTGGCAGAGGGAAAGC
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 ACTGGCTCACGGGATGACCTGTACCGTGTCCAGAAAGTGGCAGCCTCTGATCGTACAGG
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 GCAATGTTCAAATACATTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT
 AAGACTATTACAGT**TAA**ATTAGAATGCTCCAATGTTCTGCTTCGAAATAACCTTATTA
 AAAGATTTTTTGCAGGAAGATAGGTATTATTGCTTTGCTACTGTTAAAGAAAACAA
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 ATCAAAATTGGCAGAAAACACAAATATGTCATATATCTTTTTAAAGTATTCA
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 GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACCTCCAGCACCTAATGGAACCACATT
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 TACTTTATTCTGTCTGCCCTCAATAATATCACAAACAATATCCAGTCATTAAATGGC
 TGCAATAACTGATCCAACAGGTGTAGGTGTTAGTGTGAGCACTCAATAAATA
 TTGAATGAATGAACGAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRGRAQPPLLPLSLLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPPDTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSLKRDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPELPSFYMTP
 SHRQVVFEGDSLPGQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGCHVQTKRGNNRTVDIVVLESSAQYCPPERVVNNKGDFRPRTLAGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPLNL
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRTKEEKSKELGDMVDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596**N-myristoylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

FIGURE 17

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCCTGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTGGAAAAAGAAAACATTCGTCTTTGGAGAACAGATTA
TTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATTTATTGGAAAAGGATCTCAAAAAA
TCATGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTGTGTGTGTTGAT
GGAGAGTAGCTTAGTATCTTCATCTTTGGTCACTGTCCTTTAAACTTGATCA
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TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAACGACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACAC
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQQLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGQSQKS

Signal peptide:

amino acids 1-21

FIGURE 19

CTGTCGTCTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTTTACAGCCTGTT
 CAAAGTGTGGCTTAATCCGTCTCCACCACCAAGATCTTCTCCGTGGATTCCCTCTGCTAAGACC
 GCTGCC**ATG**CCAGTGACGGTAACCCGACCACCATCACAAACCACAGACGTATCTCGGG
 CCTGGGGTCCCCCATGATCGTGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTCGC
 CTGCTGCAGCTGGTGTCTACCTGCCTGCCTCGCTGGTAGCGTGGCGCTGGAC
 GGGGTCCATGGCAACTGGTCCATGTTACCTGGTGCTTCTGCTTCTCGTGAACCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTTCCCCCTGCTTGGCGCAACTCCCC
 ATCACCTTCGCCTGCTATGCGGCCCTTCTGCCTCTGGCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCCTGTCCCACGGCCGTTCGCGGGACCACGCCATGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGCCGGCCGGCGAG
 ATCACTGGCTATATGCCACCGTACCCGGCTGCTGAAGGTGCTGGAGACCTCGTTGCCTG
 CATCATCTTCGCGTTCATCAGCGACCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTATCCTAGCGGCCATGCCATCCTGCTGAACCTGGGG
 GAGTGCACCAACGTGCTACCCATCCCCCTCCAGCTTCTGTGGCCCTGGCTGTGTC
 TGTCCCTCTATGCCACCGGCCCTGTTCTCTGGCCCTCTACCAGTTCGATGAGAAGTATG
 GCGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCACTACGTGTG
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCACCTACTGGCGTATGTGGC
 TGACCTGGTGCACTCTGCCACCTGGTTTGTCAGGTC**TAA**AGACTCTCCAAGAGGCTCC
 CGTTCCCTCTCCAACCTTTGTTCTTGCCTGGCCGAGTTTCTTATGGAGTACTTCTTCC
 TCCGCCTTCCTCTGTTCTCTGCCCTGGCTCTCCCTCCACCTTTCTTCCCTTCC
 CAATTCCCTGCACTCTAACCAACAGTTCTGGATGCATCTTCTCCTCCCTTCTGCTGT
 TTCCCTCTGTGTTGTTGCCACATCCTGTTACCCCTGAGCTGTTCTCTTT
 CTTTCTTCTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCAGTCAGCTCACTGCAACCCCCGCCTCTGGGTTCAAGCGATTCTCCTCC
 CCCAGCCTCCAAAGGTGCTGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTCTCTT
 TTCCACTCTCTTTCTCATCTTCTGGTTGCCCTGCGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTCTCCTGTGTCCTGGGAGCCCTGAGACTTCTCTCCTGCCCTCCA
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTGAGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCATTGCCAAAGCATGCCCTGCCACCCCTCGCTGCGCTAGTCAGTGTGAC
 GTGTGTGTGTGTTGGGGGTGGGGGTGGTAGCTGGGATTGGCCCTTCT
 CCCAGTGGAGGAAGGTGTCAGTGTACTTCCCTTAAATTAAAAACATATATATATAT
 ATTGAGGTCAGTAATTCCAATGGCGGGAGGCATTAAGCACCAGCCTGGTCCCTAGG
 CCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAATTGGCCAGGCTTACAGAACAC
 CCACTGCCAGAGGCCATCTAAAGGAAGCAGGGCTGGATGCCCTTACCCAACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTSSSGLGSPMIVGSPRALTQPLGLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTЛИLIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIАATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLTFVACI
IFAFISDPNLYQHQPALEWCVAVYАICFILAAIAILLNLGECTNVLPPIPFPSSLGALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRLAVAILTAINLLAYVAD
LVHSAHLVFKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

GAACGTGCCACCATGCCAGCTAATTGGTATTTAGTAGAGACGGGTTTACCATGTTGCCAGGCTGGTC
 TTGAACTCGTGACCTCATGATCGCTCACCTCGGCCTCCAAAGTGTGGATTACAGGCATGACCAACTGACGC
 CTGCCAGCCTATGCATTAAAGAAATTATTCTGTATTAGGTGCTGTGCTAAACATTGGCACTACAGTGACCA
 AACAGACTGAATTCCCCAAGAGCAAAGACCAAGCAGTGGAGACCAACAAGAAACAGGAATGCAAAAGAGACCA
 TTATTACTCACTATGACTAAGGGTCACAAATGGGTACGTTGATGGAGAGTGAATTGTTAAGAGACTACAGAGGG
 AGGACAGACTACCAAGAGGGGCCAGGAAAGCTCCTGTGACGAGGTGGTATTCAAGCCAAACTGGAAGAATGA
 GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGAGCACTACACTCACTACACTTGGCCTGAGAA
 AATAGCATGGATTGGAGGAGCTGGGGAACACCCTCTGCGCACCTGGGCAGGAGGCAATTGAGGCTTGAGA
 AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTGCAGGTGGAATCATTAGGTCTTATC
 AACAGATATGGCAAGCAAAGCCAGGGAGAATTGATGTTAATGCTGAGGTTGGAGCCAGGCTAGATGGGACAG
 TGGTGGGTGATGCAAAGGAAAGAGGTCAAGGAAGCAGGGCAGACGTGGGAGAAGGTGTGGGGTTGGTTCCA
 TCTTGCAGTCTGCCGAATGTGGATGGGAAGACCAAGAGGGAGCAAGGGCAGAGGGGAAGGGAATCTTAA
 AGAAGTCCTGGATGCCACACTCTTCTCCTCTCCCTCAGAGGTCTACTCGTGGTCTTCAT
 TTCCTGCCCTGCCTCCATCTCCTCTGGGTGCTGGGAAAGTGGAGGATTAGCTGAAGTTGCTTCTCAGGGCCTG
 TCTGAATCTCATTGCTTCTGGGAGGACATAATTACCTGCTCTAGCTTATCATCTTACATTCCCTGTAG
 CCACTGGGACATATGTGGTCTCTCTAGCTCCTGTCTCCCTCATGCCTTGCTGGTATGGCATGTTAG
 GGGGAAGGTCAATTGCTGTCAGAGGGCACTGACTTTCTAATGGTGTACCCAAGGTGAATGTTGGAGACACAGTC
 GCGATGCTGCCAAGTCCCAGGCACTATCCAGGAGATCGTGCCTGCCAGGTCCCTCCCTGCATGGT
 ATGCAGCCCCCTCCCA**ATG**TTCTGGCACTTTGCTCTCCCTCCGTTGCACATCCCTTGGAACTGTTCT
 GTGAGTACATGCTGGGTCTCCCCTTCTCCCTGCTCAGGTGAATCTCAGGCCCTCTCCACCCAAAGGTTC
 ACATGGATCCTAACTACTGCCACCCCTCCACCTCCCTGCACTGTGCTCCCTGCCCTGGTCCCTTACCCAGGCTTC
 TCCACCCCTCCCTATCTCAGGTATTCCCAGGTGGTGAAGGACCACTGACCTACCGCATGGCCAGG
 GCGAGTGGCTCACCTCATTGAGTGGAAAGGGCTGGAGCAAGCGAGTGACTIONCCTGCTGCCCTGGAAATCAGCCT
 TTCCCTCATTACAGACCTCAGCGAGGGCAACAAAGGGCTCGCTTGAGCAGGAGTGGCTGAGCAGTTGCCA
 TCGCGGAAGCCAAGCTCCGAGCATGGTCTTCGGTGGATGGCAGGACTCCACTGATGACTCTATGATGAGGACT
 TTGCTGGGGAAATGGACACAGACATGGCTGGCAGCTGCCCTGGAGCCTGAGAGCGACTGCTCACAGACCGTGTCCCCAGACA
 CCCGTGCTCTAGTCTGTCAGCCTGGAGGATGGGTGTTGGCTCCCCGGCCGCTGGCTCCCAGCTGCTGG
 GCGATGAGCTGCTCTGCCAAACTGCCCCCAGCCGGAAAGTGCCTCCCGAGCTGGCCACTGGAGGCCCC
 AGGACTCACTCTACAACACTGCCCTCACAGAGTCCTGCCCTCCCCCGGGAGGAGGAGCCAGCCCCCTGCAAGG
 ACTGCCAGCCACTCTGCCACCACTAACGGGAGCTGGGAACGGCAGCGGCAAGCCTCTGACCTGCCCTTCTG
 GGGTGGTGTCTTAGATGAGGATGAGGAGGCCAGAGGAACAG**TGA**CCCACATCATGCCCTGGCAGTGGCATGCA
 TCCCCCGGCTGCTGCCAGGGCAGAGCCTCTGTGCCAAGTGTGGCTCAAGGCTCCAGCAGAGCTCACAGCC
 TAGAGGGCTCTGGGAGCGCTCGCTCTCGTGTGTGTTTGATGAAAGTGTGAGGAGGAGGCAGGGCTG
 GGCTGGGGCGCATGCTCTGCCCTACTCCGGGCTTGGCGGGGGTGGCCGGGCTCTGGGCATGGCTACA
 GCTGTCAGACAGTGAATGTTCATGTTCTAAATGCCACACACATTTCTCTCGGATAATGTGAACCACTA
 AGGGGTTGTGACTGGGCTGTGAGGGTGGGAGGGGCCAGCAACCCCCCACCTCCCCATGCCCTC
 TCTTCTCTGCTTTCTCTCACTCCGAGTCATGTGCACTGCTGATAGAATCACCCCCCACCTGGAGGGCTG
 CTCCCTGCCCTCCCGAGCCTATGGGTGAGCGTCCCTCAAGGGCCCTGCCAGCTGGCTCGTGTGCTTC
 ATTACACCTCTCCATCGTCTCTAAATCTTCTCTTTCTAAAGACAGAAGGTGTTGGTCTGTTTCTAGTC
 GGATCTTCTCTCTGGGAGGCTTGGATGAAAGCATGTACCCCTCCACCTGGCCCCCTTAATGG
 GGCTGGGGCCCTTCCCAACCCCTCTAGGATGTGCGGGCAGTGTGCTGGCGCTCACAGCCAGCCGGGCTGCC
 ATTACACGAGCTCTGAGCGGGAGGTGGAAGAAAGGATGGCTCTGGTGCACAGAGCTGGACTTCATGTT
 CTTCTAGAGAGGGCCACAAGAGGGCACAGGGGTGGCGGGAGTTGTCAGCTGATGCCCTGCTGAGAGGCAGGAAT
 TGTGCCAGTGAAGTGAAGTGAAGGGAGTGTCTCTGGGAGGAAAGAAGGTAGAGCCTTCTGCTGAAT
 GAAAGGCCAGGCTACAGTACAGGGCCCGCCCCAGCCAGGGTGTAAATGCCACGTAGTGGAGGCCTGAGCAG
 ATCCCTGCATTCCAAGGTCACTGGACTGTACGTTTATGTTGTTGGAGGGTGGCTTGAATTAAGGGC
 CTTGAGGCTTGGCAGGTAAGAGGGCCCAAGGTAAGAACGAGGCCAACGGGACAAGCATTCTATATATAAGT
 GGCTCATTAGGTGTTATTTGTTCTATTAAAGAATTGTTTATTAAATTAATAAAAATCTTGTAAATCTC
 TAAA

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGPLSSLAQVNLSPESHPKVHMDPNYCHPSTSLHLCS
LAWSFTRLLHPPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALSAFSSY
SDLSEGEQEAFRAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTCCTGGCGCTGTTACACAAGCAAGATAAGCCAGCCCCACCTAATTTGTTCCCT
 GGCACCCTCCTGCTCAGTGCACATTGTCACACTTAACCCATCTGTTCTAATGCACGA
 CAGATTCCCTTCAGACAGGACAACGTGATATTCAAGTCAGTTCTGATTGAAATACCTCCTAAG
 CCTGAAGCTCTGTTACTAGCCATTGTGAGCTCAGTTCTCATCTGAAAATGGGCATAA
 TACAATCTATTCTGCCACATCAAGGGATTGTTATTCAAGGGAAAAACCAATACCAAAG
 AAGCCTACAATGTTGGCCTAGCCAAAATTCTGTTGATTCAACGTTGTTTATTCACTTCT
 ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTTT
 TTAAAACAATGGAAAATAACCTATTCTTGAAAGTGAAGCAAACCTAAACTCAGATAAA
 GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTGAATCTACCCAA
 CAGCCACGGAATAACAGATTCTCCAGTAACTCATCAGCAGAGCATTCTGGCAGTCTAA
 AACCCACATCTACCATTCCACAAGCCCTCCCTGATCCATAGCTTGTAAAGTGCCT
 TGGAATGCACCTATAGCAGATGAAGATCTTGCCCATCTCAGCACATCCAATGCTACACC
 TGCTCTGTCTTCAGAAAACCTCACTGGTCTTGGTCAATGACACCGTAAAACCTCCTGATA
 ACAGTTCCATTACAGTTAGCATCCTCTTCAGAACCAACTCTCCATCTGTGACCCCTTG
 ATAGTGAACCAAGTGGATGGCTTACCAACAGTGAAGTAGCTTCACTGGTTACCCCTTA
 TCAAGAAAAACAACTCTACAGCCTACCTTAAATTCCAATAATTCAAAACTCTTCAA
 ATACGTCAAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTGGGCCATTAGGT
 GCTATTCTGGGTGTCCTTGCTACTCTGTGGCTACTTGTGTGGAAAAGGAAAAC
 GGATTCAATTCCCCTCGGCGACTTATGACGACAGAAATGAACCAAGTTCTGCGATTAGACA
 ATGCACCGGAACCTTATGATGTGAGTTGGAAATTCTAGCTACTACAATCCAACCTTGAAT
 GATTCAAGGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
 TCCACTTCGTACTCTGTATAGAACTAACAGCAAAAGGCCTAACAGCAAGTGTCACT
 CATCCTAGCCTTTGACAAATTCACTTTCAAAAGGTACACAAAATTACTGTACGTGGAT
 TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAAGGTTTCTTCTACAATTGGCCATCCTGAGGCATTACTAAGTAGCCTTAATT
 TGTATTAGTAGTATTCTTAGTAGAAAATATTGTGGAATCAGATAAAACTAAAAGATT
 TCACCAATTACAGCCCTGCCTCATAACTAAATAAAAAATTATTCCACCAAAATTCTAAA
 ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCAATTCAAGATTGCAT
 TTTCTAAATGAAAATTGAAAGGGTGTGTTAAAGAAAATTGACTTAAAGCTAAAAGAG
 GACATAGCCCAGAGTTCTGTTATTGGAAATTGAGGCAATAGAAATGACAGACCTGTATT
 TAGTACGTTATAATTCTAGATCAGCACACATGATGCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGCCATGGCAGGAAAGCTGACCCCTACCCAGGAAAGTAATAGCT
 TCTTAAAGTCTCAAAGGTTGGAAATTAACTGTCTTAATATATCTTAGGCTCAA
 TTATTGGGTGCCTAAAAACTCAATGAGAATCATGGT

FIGURE 24

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNNSAEHSLGSLKPTSTISTSPPPLIHSFVSKVPWNA
PIADEDELLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTSNDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLLTIVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNSA
MPESEENARDGIPMDDIPPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**ATG**GTAAAATCGCCTTCATAACCCCTACCGCCGTGCAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTCATTCATCTGGCAGGACTTATTGTTGGAGCCTGCATTACAAGTACT
 TCATGCCAAGAGCACCAATTACCGTGGAGAGATGTGCTTTTGATTCTGAGGATCCTGCA
 AATTCCCTCGTGGAGGAGAGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTCTGTGATAGTGACCCCTGCAG
 CAATTATTGACTTTGAAAAGGAAATGACTGCTTACCTGGACTTGTGCTGGAACTGC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTGATGTTAGTAACCTTGGCATCTTACCAACTTGCAATAACAGA
 AAGTCCTTCCGCCTCGTCGCAGAGACCTCTGCTGGTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCTGGTAATAAGAAGTCAGAGATTACAATATGACTTAA
 CATTAAGGTTATGGGATACTCAAGATATTACTCATGCATTTACTCTATTGCTTATGCTTT
 AAAAAAAGGAAAAAAAAAAACTACTAACCAACTGCAAGCTTGTCAAATTAGTTAAT
 TGGCATTGCTTGTGTTTGAAACTGAAATTACATGAGTTCATTGCTTGCATTATAG
 GGTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC
 GTGTTTTTTGTTGTTGTTCTTTCTTTAAGTAAGCTTGTCAAATTAGTTAAT
 GTGGAGCAATTAAAATTGAAATATTAAATTGTTGAACTTTGTGAAATTATA
 TCAGATCTCAACATTGTTGGTTCTTTGTTCTTCAACTTGTACAACCTTGTAAATTAGA
 ATTACATCTTGCAGTTCTGTTAGGTGCTCTGTAATTAACTGACTTATATGTGAACAAATT
 TTCATGAGACAGTCATTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTTAGGTGCTGAATGCTGAAAGGAGTTAGGTTGTATGAATTCTACAA
 CCCTATAATAAAATTACTCTATACAAAAA

FIGURE 26

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCMILLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDPAAIIHDFEKGMTAYLDLLLGNCYLMPNNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFYQLCNNRKSFRRLRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCAGCCAGAGCAGCCCCGGGACACCAGCACGGACTCTCT
 CTTCCAGCCCAGGTGCCCTTCACTCTCGCTCCATTGGCGGGAGCACCCAGTCCTGTACGCC
 AAGGAACCTGGTCTGGGGCACC**ATG**TTTCGGCGGAGCCCCAGCCTCATCCTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGCCAGCCCACAACCCTGGGG
 GGCCCATCACCCCCCACCAACTTCCTGGATGGATAGTGGACTTCTGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTCTGCTGATGTTATCGTCTGTGCCCGGTCA
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTCCCCAAGAACAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGCCCTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCGAGGAAGCCCTGGATTCCCTCCGGCAGCTCCAGGCCACATCTGGCCG
 CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGCGGTGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGACCAAGGAAGTCCA
 GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGTCCTTG
 AGGGGCTGTGGTGGCCGGTGAGGGCAAGGGAGCTGGAAGGGCTCTCTGTTAGCCCAG
 GAAGCCCAGGGACCAGTGGTCCCCCGAAAGCCCTGTGCTGCAGCAGTGTCCACCCAG
 TGTC**TAA**CAGTCCTCCGGCTGCCAGCCCTGACTGTGGGCCCTCAAGTGGTCACCTCCCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTCCTGACACTCCCTCCTGGCCTCCCTGTGG
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTCCCCGG
 GGAATCTTACCAAGTGCATCATCCTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGTGGATTACAGGCGTGAGCCACCGTGCCGGCCAAACTACTTTAAAACA
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTCCTGAAGG
 TGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGGCATTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGTGAGTTCTCATCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAACCTTCCTGTCTGGCCTCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTGAGGGACCTCCACCCCTGGGAAGTCCGAGGGCTGGGGAGGGTTCTGACG
 CCCAGCCTGGAGCAGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
 TGTCCACAATATCGTCAGTCCTCGACAGGGAGCCTGGCTCCGTGCTTCTGAGGAGGCT
 CTGGCAGGAGGTCCTCTCCCCCATCCCTCCATCTGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACAATAACCTTATTCCGGCCTGAAAAAAAAGA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 28

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
>subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEKGSQEGDQEVTQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLQAQEAQGPVGPPESPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGACTCGGAAGGAGGAGCAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAG**ATG**
 AAGTTCCAGGGGCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGCAGTGGGAGGCTGG
 CCCCTGCAGAGCGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGGCC
 TGGGAGACGCCCTGAGCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTGGCCAAGGGACCAGAGAACAGCTGGCACTGGAGTCAG
 GCAGGTTCCAGGCTTGGCGCAGCAGATGCTTGGCAACAGGGTCGGGAAGCAGGCCATG
 CTCTGGAAACACTGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCA
 GATGCTGTCCGGCTCCTGGCAGGGGTGCCTGGCACAGTGGTGGCTTGGAAACTCTGG
 AGGCCATGGCATTTGGCTCTCAAGGTGGCCTGGAGGCCAGGGCAATCCTGGAG
 GTCTGGGACTCCGTGGTCCACGGATACCCCGAAACTCAGCAGGCAGCTTGGAAATGAAT
 CCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGGAGGCCACCAAACCTTGGACCAACAC
 TCAGGGAGCTGTGGCCCAGCCTGGCATGGTCAGTGAGAGGCCAGCAACCAGAACATGAAGGGT
 GCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGAGGCAGCGGC
 TCACAGTCGGGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTGG
 TGGCAGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGA
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGA
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGA
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGA
 TCCAGCACCGGCTCCTCCGGCAACCACGGTGGAGCGGGAGGAAATGGACATAAAC
 CGGGTGTAAAAGCCAGGAATGAAGCCCGCGGGAGCAGGGAAATCTGGATTAGGGCTTCA
 GAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCTGG
 GGCTCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGGAGTCATACTGTGAACCTGAGACGTCTCCTGGATGTTAACTTGA
 GACTCTCGCATCCCG**TGA**CCTCCAGACAAGGAGCCACCAGATTGGATGGAGCCCCACACT
 CCCTCCTAAACACCACCCCTCTCATCACTAACTCAGCCCTGCCCTGAAATAACCTTA
 GCTGCCCAACAAAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAAA
 AAAAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAAA

FIGURE 30

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPSGSGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSGSSGSSGGSSGGSSGGSGSNGSRGDGSESSW
GSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL
GGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGMNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGTGTCAACCG
 TGCCCTGGCTGGAGTTCTCTCCTTGCTGACCATTGTTCCCTGCTGGAATATTACCGGGACATCTTCA
 CTCTCCTGCTGCCCTGACCGGAGCTTGGTGTGCGAGAGACTGAGGGAAAG**ATGT**TTCCTGAACAAGC
 TGCTGCTACTTGCTGCTGGCTGGCTTCCAGATTCCCAGTCCCTGAGGACTTGTCTTCTGGAAGAGG
 GTCCCTCATATGCCTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTGGACATAKGCCCTGTGGTGACCAGC
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGAAACTGCTCGCTCGTGGGTGTCAAGGAGTAGTG
 GACGGAGTGGGGCTTCATGAGAAAATCACCCCCACCACCTACCAACAGCCCTGGGAGGCCAGCCTCCCAGACCA
 GCCAGGGCTGCAGGCACAGCTGCCAGGCCCTTCCACAACCAGCCCTCCTGCGCCGGACCCTAGAGT
 TCGTGGCAGAAAGAATTGGATCAAACATGTGTCAAACATATCAAGGCTACACTGTTGGCAGATCTGGTGCGCCAGG
 CAGAGTCACTTCTCCAAGAGCAGCTGGTACACAGGGAGAGGAAGGGGGAGACCCAGCCAGCTGGAGATCT
 TGTGTTCCCAGCTGTGCCCTCACGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG
 GGGCTGTGCCCGCTGCTCCAGAGGAGACCCGGCAGGCCATTGAGCAGTCAGAGAACATTGCTGTGGGGC
 TTGCAACAGAGAAAGCCTGTGCTGGCTGTGAGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTCGCACACTTCGAGCCCAGGGCCTGAACCTGCTGCCGGGGAGCGGAGGGGCTGCTCCCGCC**TGAC**
 GTGCTCTCTGGCCGTGGGCCACGGGACCCGTACGAGGGAGTCTCCCAGAGCATCTGGAACAGCTCCTAGGC
 CAGCTGGGCCAGCCTGCCAGTCCCTGTGAGCAGCAGTGGCAAAGTGTCTGTG
 GAGTTAGCTCCCTCTCGTGCAGATCAAATTCTATCTAGGGCCCCGGCACAGTACAGGCTGGAGAGAGGG
 CAGGCTCGAAGGCTCTGCACATGCTGCTTCCTGTGAGAAGAGACTTCAAGGGCCGGTCCGCTGCAGCTG
 CTGCTGAGCCAAAGAAATGTGGGGCTTCTGGCAGACACAAGGCAAGGGAGTGGACTTGTCTATTCTTCTA
 CGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCTGCCAGGCCACCAGGCCAG
 TGGCCAGGGACTTGTGAAGAATTAGCAACACTGTCTAATCTGTTCTAGCCGAGGCCACCTGCCAGAACCC
 CAGCTAAGAGCCTGTGAGTTGGTGCAGGCCAAACCGGGGCACTGTGCTGCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCTTGGGCATTGCACCAAGAACCTGGACCCCCGCTCACGAGGAGGCCAAGTGCCTGAGACCCCTCAC
 TGGTTGGGTGTAGCTGGTCTACAGTCAGACTTCTCTGCTTAAGGGTGTCACTGCCCTGGCATCCCACACGCGA
 ATCCTAGAGGAAGGAGAGTTGGCCTGATTGGGATTATGGCAGAAAAGTCAGAGATGCCAGTCCTGGAGTAGAA
 GAGGTGGTGTGTTATCTCTGGACTAAATGAAATGAGGTGTGTTGCTGCTCAACACAGAAATTCAAGCCT
 CATTGCTATCCCAGCATCTCTTAAACTTTGTTAGTCTTGAAGGACTTCAAGGCAATGACTCCTGCTTAAC
 TTATGAAGAAAGTTAAACATGAATCTGGGAGTCTACATTCTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT
 ATAATGCCTAACACAGGCCGGTCTGGGCTCATGCCGTAACTCCAGCACTTGAGAGGCCAGGGCG
 GACTGCCAGGTCAAGGCAATTCAAGACCAGCCGGCAACATGGAAAACCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGCATGGTGGTGTGCTGTAACTCCAGTACTCAGGAGGATGAGGCCAGGAGACCTGCTGAAC
 CTGGAGGTGGAGGTTGCACTGAGCCAGGTCGACACTGCACTCCAGTCTGGTAACAGAGCGAGACTTTCTAG
 AAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCCCTGTACCTTCAGCCCTG
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTAGAGCTTTTAA
 CTGGTTTCTTAAAAAAGGGCGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 TTTTTTTTTTTTAAAGGGCTTTATTAAAATTCTCCCCACAGATGGCTCTGCAATCTGCCACAGCTC
 TGGGGCGTGTCTGTAGGGAAAGGCCCTGTTTCCCTGAGGCGGGCTGGCTGTCCATGGGTCCGGAGCTG
 GCCGTGCTGGGCCCTGGCGTGTCTAGCTGCTTCTGCGGGCACAGAGCTGCCGGCTGGGGCACCAGGG
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGTCTTAAACCGACCCGTAGGTGCTCTGAGATGCTG
 GGTCCACCCCTGAGTGGCACGGGAGCAGCTGGCGGGTGTCTCYTAGGCCAGTCTGGGAAACTAAGCTC
 GGGCCCTCTTGCAAAGACCGAGGATGGGTGGGTGAGGGACTCATGGGAATGCCCTGAGGAGCTACGTGT
 GAAGAGGGCGCCGGTTGGCTGAGCGGGCTGGAGGCCCTCTGCCCTGAGGCTCAGTTCCCTTCCGTCTA
 ATGAAGAACATGCCGTCTGGTGTCTCAGGGCTATTAGGACTTGGCCCTCAGGAATGGCCATGTCCTCTGCTGCGTGGAC
 GTTATTTCACAACGTCTCGCAGGTTGGCTGGCAGGTGGCAGCTCATGGGAATGGCCATGTCCTCTGCTGCGTGGAC
 GTCGCGGTGGAGTGGCAGCCAGGGGGCCAGACGTGCGCTGGGGTGAAGGGAGGCGCCCGGAGGG
 CCTCACAGGAAGTGGAGGCTCCGCACACCAGGAGGGGGCTCCGCCGCCGCCACCACCGTCCAGG
 GGCGGTAGACAAAGTGGAGTGGCTGGCTGCGCTGCGCAGCAGGTAGCCCTTGTATGCAGTGCAGGCCGCG
 TCGTCCGCCAGCTGGAGCAGGCCGTCCACAGCACGAACAGCCGGTGCAGCCT

FIGURE 32

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTSLGAQPSQTSQLQALQAFFHNQPP
SLRRTVEFVAERIGSNCVKHIKATLADLVRQAESLLQEQLVTQEEGGDPAQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTCGGGGTCACTGAAGGCAGTCTTGATCAGGAAACTG
AAGACTCTCTGCTTTGCCACAGCAGTCAGCTGCAGCTCCTGAGGTGTGAACCCACATCCC
TGCCCCCAGGGCCACCTGCAGGACGCCACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
AGTAGCAACAAAGAGCAGCGGTAGCAGTGTCTGATCCTCTTGCCCTCATCACCATCCT
CATCCTCTACAGCTCAACAGTCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA
GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
AACAAAGACACTGCCCTCTCGGTGCCACCAGTGTGATTGTCAGCAGCTCCAGCCACCTGCT
GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGATGAATGATGCAC
CCACCACTGGCTACTCAGCTGATGTGGCAACAAGACCACCTACCGCGTGTGGCCATTCC
AGTGTGTTCCCGTGTGAGGAGGCCAGGAGTTGTCACCAGGACCCCTGAAACCGTGT
CATCTTCTGGGGGCCCGAGCAAGATGCGAGAACGCCCCAGGGCAGCCTCGTGTGATCC
AGCGAGCGGGCCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCCGATGCGG
CAATTGACGACCTCTCCGGGTGAGACGGCAAGGACAGGGAGAAGTCTCATTGTT
GAGCACAGGCTGGTTACCATGGTATCGCGGTGGAGTTGTGACCACGTGCATGCTATG
GCATGGTCCCCCCCCAACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
TACGAGCCCAAGGGGCCGGACAATGTGTCACCTACATCCAGAATGAGCACAGTCGCAAGGG
CAACCACCAACCGCTTCATCACCAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA
TCACCTTCTCCCACCCCTCTGGAC**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
AGGAGAACGAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTCTGGCCAATCAAGGCTTG
CTGGAGTGTCTCCAGCCAATCAGGGCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCC
TGGGAATCTGTTGGGAATCAGGGATTGGGAGTCTATGTTAATCAGGGGTCTTTC
TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTCTGAGTCATCTG
AGGCTAAGGACATGTCCTTCCATGAGGCCTGGTTAGAGCCCCAGGAATGGACCCCCCA
ATCACTCCCCACTCTGCTGGATAATGGGGCTGTCCCAGGAGCTGGAACTTGGTGTG
CCCCCTCAATTCCAGCACCAAGAGAGATTGTGTTGGGGTAGAAGCTGTCTGGAGGCC
GGCCAGAGAATTGTTGGGTTGTGGAGGTTGTGGGGCGGTGGGGAGGTCCCAGAGGTGGGA
GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTGGACAAACCTTCCCCCTCTGGG
CACCTCTGCCACACCAGTTCCAGTGCAGGAGTCTGAGACCCCTTCCACCTCCCTACAA
GTGCCCTCGGGTCTGCTCTCCCGTCTGGACCCCTCCAGCCACTATCCCTGCTGGAAGGCT
CAGCTCTTGGGGGTCTGGGTGACCTCCCCACCTCCCTGGAAACTTAGGGTATTTGC
GCAAACCTTCAGGGTGGGGACTCTGAAGGAAACGGACAAAACCTTAAGCTTTCT
TAGCCCCCTAGCCAGCTGCCATTAGCTGGCTCTAAAGGGCCAGGCCTCTTCTGCCCT
CTAGCAGGGAGGTTTCCAACCTGTTGGAGGCCCTTGGGCTGCCCTTGTCTGGAGTC
CTGGGGCTCCGAGGGTCTCCCTGACCCCTCTGCTGTCCTGGGATGGCTGTGGAGCTGT
ATCACCTGGGTCTGCTCCCTGGCTCTGTATCAGGCACATTAAAGCTGGCCTCAGTGG
GGTGTGTTGTCTCTGCTCTGGAGCCTGGAAGGAAAGGGCTCAGGAGGAGGCTGTGA
GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGACACTGGGTGATGGTGG
GGCGGTGACTGCCCAAGACTGGTTGTAATGATTGTACAGGAATAAACACACCTACGC
TCCGGAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSAVFVILFALITILYLSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCVIVSSSHLLGTKLGEIERAECTIRMNDAPTTGYSADVGNKTYRVVAH
SSVFRVLRRPQE VNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVVYGMVPPNYCSQRPRQLQRMPYH
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT
 GAGGGAAAGCATTCCCTAGCTGTGGCGCAGAGGGCGAGGCTGAAGCCGAGTGGCCGAGGTGTCTGAGGGCTG
 GGCAAAGGTGAAAGAGTTCAAGAACAGCTCTGGAACCCATGACCCATGAAGTCTTGTGACATTATAACCGT
 CTGAGGGTAGCAGCTGAAACTAGAAGAAGTGGAGTGTGCCAGGGACGGCAGTATCTCTTGTGACCCCTGGC
 GGCCTATGGGACGTTGGCTTCAGACCTTGTGATACACC**ATG**CTGCGTGGGACGATGACGGCTGGAGAGGAATG
 AGGCCTGAGGTACACTGGCTTGCCCTCTAGCCACAGCAGGCTGCTTGACTTGAACGAGGTCCCTCAG
 GTCACCGTCCAGCCTGCGTCCAGAAGCCCAGGCACTGTGATCTGGCTGCGTGGTGGAGACCTCCA
 AGGATGAATGTAACCTGGCGCTGAATGAAAGGAGCTGAATGGCTGGGACGATGCTGATCTGGCTGCGTGGTGGAGACCTCCA
 CACGGGACCCCTCGTCATCACTGACCAACACTAGCTGGGACGCTGGGACGATGCTGCTGCGTGGTGGAGACCTCCA
 GGGCTGTGGCCAGCGTGCAGCCACTGTGACATAGCCAATCTCAGGACTTCAGTTAGATGTGACGACGTG
 ATTGAAGTGGATGAGGGAAACACAGCAGTCACTGGCTGCACCTGCCTGAGAGGCCACCCAAAGCCCAGGTCCGG
 TACAGCGTCAAACAAGAGTGGCTGGAGGCTCAGAGGTAACACTACCTGATCATGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGGCCAGGAGGACGAGGGCATGTACAAGTGTGACGCCCTACAACCCAGTGACCCAGGAAGTGAAC
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCGATCATCTACCCCCCAGAGGCC
 CAAACCATCAGCTCACCAAAGGCCAGAGTCTCATTCTGGAGTGTGGGACGCTTACAGGCTGAGGATGCTGCG
 ACCTGGGCAAGGATGGGCTCAGTGTGACCCGGTACAACAAAGACGCGCTTCTGAGGACAACTCCTCATCGAC
 ACCACCAAGCGAGGAGGACTCAGGACACTACCGCTGCATGGCGACAAATGGGTTGGGAGGCCGGGGCAGCGGTC
 ATCCTCTACAATGTCCAGGTGTTGAACCCCCCTGAGGTACCATGGAGCTATCCCAGTGGTATCCCCTGGGGC
 CAGAGTGCCAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTG
 CTCATCTCCAGGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGCAGCATGGGCGCTGAGGACGAAGG
 GTCTACCAAGTGCATGGCGAACAGAGGTTGGAGGCCATGGCGTAGTGGCAGCTGCGGACCTCCAGGCCAAGC
 ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATCACCTCCAAACTCGGCCAAC
 CCTGAGCAGATGCTGAGGGGGCAACCGGCCCTCCCCAACGCCCCAACGTCAGTGGGGCTGCTTCCCCGAAGTGT
 CCAGGAGAGAAGGGGCAAGGGGCTCCGCCAGGGCTCCCATGAGGGCAGTGGCGGGGCGCAATCTCTACTATGTGG
 TAAACACCGCAAGGCTCACAAATTCTCTGACGATTGGACCATCTCTGGCATTCCAGCCAACCAGCACGCC
 ACCAGACTTGAACCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTAACACTGTGCGGGAGAGGGCCAGACAGC
 ATGGTCACCTTCCGAACTGGACGGGGCCAAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC
 GACCCCTGGAGGCAAGTCCCCAGAGCAGCAGGCCAACACGCCCTCTCCCCCGAGAAGCTCCGACAG
 CCCACCATCTCCACGCCCTCCGAGACACTCAGTGTACGTGACCTGGTGGATTCTGGGCAACAGCGCC
 CAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGAGACTGGATTCTGGCACCAGCGCC
 TCGGGCTGTCGTGGAGATCACGGCCTAGAGAAAGGACCTCTACAAGTTGAGTCCGGCTCTGAACATG
 CTGGGGAGAGCGAGCCCAGCGCCCCCTCTGCCCTACGTGGTGTGGCTACAGCGGTGCGTGTACGAGAGG
 CCCGTGGCAGGTCTTATATCACCTCACGGATGCGGTCAATGAGACCACCATGCTCAAGTGGATGTACATC
 CCAGCAAGTAACAAACACCCCAACTCATGGCTTATATCTATTATGACCCACAGACAGTGGACAAATGATAGT
 GACTACAAGAAGGATATGGCAAGGGGACAAGTACTGGCACCTCATGAGGACCTCAGGCCACCTGCGAGAGAC
 GACATTAAAGATGCACTGCTTCAATGAAGGAGGGAGAGCGAGTTGAGCAACGTCAGTGTATGCTGTGAGAC
 CGGAAGTCTCTGGCCAGCCTGGTCAGTGCCACCCCCAACCTCTGGCCCACACGCC
 ATAGAGCGGCCGGTGGGACTGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGGGCTGTC
 CTGGGCTCCATGTTCTCATCGTCACCTCATCCCCCTCTGCTGTGGAGGGCTGGTCAAGCAAAACAT
 ACAACAGACCTGGTTTCTGAACTGGCCCTCCACCCCTCGCCGTATACTATGGTGGCCATTGGGAGGACTC
 CCAGGCCACCCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
 AATAGGGGCTGCCCTCGGCTCAGTGGCTACCCGGCATGAAGCCCAAGCAGCACTGCCAGGCAGCTTCA
 CAGCAGAGTGACACCAGCAGCCTGAGGCAAGCCATTTGGCAATGGATATGACCCCCAAAGTCACCAGATC
 ACGAGGGTCCAAGTCTAGCCGGACGAGGGCTTTCTTATACACACTGCCGACGACTCCACTCACCAGCTG
 CTGAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGC
 CCCACAGTCTGCTGGAAAGCAGTGTGGACCCCTCCATTCACTCAGGGCCCCCATGCTGCTTGGGCC
 CCAGTGTGGAGGGTGGACAGTCTCTGCCAAGTGGAGTGGAGAGACTGGTGTCCCCAGC
 GCCTACGTAGGGACAGGAACCTGGAATGCACTGGCTCCAGGGGGCAGTGGCGTGTCTTGA
 AAACACCCACTCTCACAAATT**TAG**GCAGAAGCTGATATCCCAGAAAGACTATATTTTTTTAAAAAAA
 AGAGACAGAGAAAATTGGTATTATTTCTATTATAGCCATATTATATATGCACTTGTAAATAATGTA
 TATGTTTATAATTCTGGAGAGACATAAGGAGTCCTACCGTTGAGGTTGGAGAGGAAAATAAAGAAGCTGCCA
 CCTAACAGGAGTCACCCAGGAAAGCACCAGCAGGCTGGCGGGACAGACTCTAACCTGGGCCCTGCA
 GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCCAGGCACATGGTT
 TGAGGGAAACAGCAAGGGCAGGTATCACAGCCTGGAGACACCCACAGATGGCTGGATCCGGTAC
 ACATTTCTTAAGATGCCCATGAGAACAGACCAAGAGATGTGACAGCACTATGAGCATT
 CAATAATCGTGGCAACATATCTGTAAAAACAAACACTGTAACCTCTAAATAATGTTAGTCT
 CCCCCCTGTAAAA

FIGURE 36

MLRGTMATWRGMRPEVTIACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVLGVVEPP
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRSTAEEAARIIYPPEAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCERGNPPPSVLWLRNAVPLISSQLRLS
 RRALRVLSMGPEDEGVYQCMAENEVGSAAVQQLRTSRPSITPRLWQDAELATGTPVSPSK
 LGNPEQMLRGQPALPRPPTSGPASPCKCPGEKGQGAPAEAPIIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRGRRPKPEIMASKEQQIQRDDPGASPQSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWI PRGNGGFPIQSFRVEYKKLKVGDWILATS AIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPS RPYVVSGYSGRVYERPVAGPYITFTDAVNETT IMLKWMYIPASNNNT
 PIHGFYIYYRPTDSDNDSDYKKDMVEGDKYWH SISHLQPETSYDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
 II VTFIPFCLWRAWSKQKHTDLGFP RSALPPSCP YTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSG
 PPCCGLGLVPVEEVDS PDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVS FETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGTCGTATGATCCGGACCCATTGTCGGCCTCTGCCCATGCCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCCCGCGAAC**ATG**CAGCCCACGGGCCGAGGGTTCCCGCG
 GCTCAGCCGGCGGTATCTGCGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCCAGC
 CCGTAACCCGCGGGAGACCACGCCGGCGCCCCAGAGCCCTCTCCACGCTGGCTCCCC
 AGCCTCTTACCAACGCCGGGTGTCCCCAGGCCCTCACTACCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCTGGACCTCGGGTCGCGCGAGGCCCTGATGCGGAGTTCCACTCG
 TGGACGGCCACAATGACCTGCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTATGCCAGTCCCAGGACCAGACTGCCGTGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAACCTGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCGCAGTTCTATGTGCTGGGGTGCCT
 ACCTGACACTTACCTCACCTGCAGTACACCAGGGCAGAGAGTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTCAAGGGATTGACAAGCTTGAGAAAGTAGTAGAGGGAGTTGAA
 CCGCCTGGCATGATGATAGATTGCTATGCATGGACACCTGATAAGAAGGGCCTGG
 AAGTGTCTCAGGCTCTGTGATCTTCTCCACTCAGCTGCCAGAGCTGTGTGACAATTG
 TTGAATGTTCCCGATGATATCCTGCAGCTCTGAAGAACGGTGGCATCGTGTGACACT
 GTCCATGGGGTGCAGTGCAACCTGCTGTAACGTGTCCACTGTGGCAGATCACTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATGGGATTGGTGGAAATTATGACGGACT
 GGCGGTTCCCTCAGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTCAAGGTGTCTCGTGGAAACCTGCTGCCGGTCT
 TCAGACAAGTGGAAAAGGTGAGAGAGAGAGCAGGGCGAGAGCCCCGTGGAGGCTGAGTT
 CCATATGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATGGGCTCCCTGGAGGTCCTCAAATGCC
 CCCCATACCTTGTCCAGGCCTTGTGGCTGCCACCATCCAACCTCACCCAGTGGCTC
TGCTGACACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCCT
 AGTCATTACAAGCATATGCTGAGAATAACATGTTACACATGGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRRLLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPLGLTTPGTPKTLRGRQAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLAQIGVXGGHSILDSSLSVLRSFYVLGVRYLTLCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYGQLSTSCH
SHLVPQNGHQATHLEVTKOPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLCS
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCGGCTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTGGTGGCTGTGGTCGGTGTGCTGGTCCCCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGCCACCTTATAGAAACATCAGTGGCACA
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCAGGCCA
 GTGCCTGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTCATATTGTCATCTACCTGTCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCCTGATGCTGGTGGACCCCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCTCGATGGCACAAAGATGCTCAGC**TAG**ATGGGCTGG
 TGTGGTTGGGTCAGGCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTCCCTCGGTTCCAGTCTTCCCTTAAAAGCCTGTGGCATTTCCTCCTT
 CTCCCTAACCTTAGAAATGTTGACTTGGCTATTGATTAGGAAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTCTTCTTGGGCTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTGAGGCGGCCTCAGGAGTGGATGCGATCTGTCCTGGCTCCACTCTG
 CCGCCTCCAGCTCTGAGTCTGGATGTTACCCCTGGAAAGATAAAGCTGGGCTTCA
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTGAGCATGTGTTCTTCAGTGTG
 GTTCTTATCACCACCTCCCTCCAGCCCCGGCGCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGAGAGCTGGGCCCCCTGAGCCCAGTGGCTTCAGGGTGCAGTGG
 AGCTGGTGGTCGCTGTCCTGCACTTCGCACTGGGCATGGAGTGCCATGCATACT
 CTGCTGCCGGTCCCTCACCTGCACTTGAGGGCTGGCAGTCCCTCTCCCCAGTGTG
 CACAGTCACTGAGCCAGACGGTCGGTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCTGTACTTGGGTTGCCCTTGTCCCTGAACCTCGTTGTAACAGTGCATGGA
 GAGAAAATTTGTCTCTTGTCTTAGAGTTGTGTAATCAAGGAAGCCATCATTAAATTG
 TTTTATTCTCTCA

FIGURE 40

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHYNQNVSQKDCNCLHVVEPM
PVPGHDVEAYCLLCECRYEERSTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTTGGGTCCGCTAATTCTGCCTGAGCGTGAGACTGAGTCATAGGGCCTGGGTCCCCGA
 ACCAGGAAGGGTGAGGGACACAATCTGCAAGCCCCCGCGACCAAGTGAGGGGCCGTGTTGGGTCCCTCCC
 TCCCTTGCATTCCCACCCCTCCGGCTTGCCTTGCCTGGGGACCCCTCGCCGGGAGAT**ATG**GCCCGGTTGATG
 CGGAGCAAGGATTCGTCTGCTGCCTACTGGCCGGTGTGATGGTGGAGAGCTCACAGATCGGCAGT
 TCGCAGGCAAACTCAACTCCATCAAGTCTCTGGGGGGAGACGCCTGGTCAGGCCCAATGATCTGCG
 GGCATGTACCAAGGACTGGCATTGGCGAGTAAGAAGGGCAAAACCTGGGCAGGCCTACCCCTGTAGCAGT
 GATAAGGAGTGTGAAGTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATGGCCTGCATGGTGTGCGGAGA
 AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCAAGTACCCGCTGCAATAATGGCATCTGTATCCAGTT
 ACTGAAAGCATCTTAACCCCTCACATCCCGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
 TCAAACCATGACTGGGATGGCAGAATCTAGGAAGACCACACTAAGATGTACATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTGCTGTGCTCGTATTCTGGACCAAAATCTGCAA
 CCAGTGCCTCATCAGGGGAAGTGTACCAAACACGCAAGAAGGGTCTCATGGCTGAAATTTCAGCGT
 TGCAGACTGTGCGAAGGGCCTGTCTGCAAAGTATGGAAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
 TGTCAGAAAATT**TGA**T CACCATTGAGGAACATCATCAATTGAGACTGTGAAGTTGTATTTAATGCATTATAG
 CATGGTGGAAAATAAGGTTAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA
 AAAGGGAGAAAGAAAATGAACTGAATAGATTAGAATGGTGACAAATGCACTGCAGCCAGTGTGTTCCATTATG
 CAACTTGTCTATGTAATAATGTACACATTGTGAAAATGCTATTATAAGAGAACAGCACACAGTGGAAATT
 ACTGATGAGTAGCATGTGACTTCCAAGAGTTAGGTTGTGCTGGAGGAGGGTTCCCTCAGATTGCTGATTG
 TTATACAAATAACCTACATGCCAGATTCTATTCAACGTTAGAGTTAACAAAATACTCCTAGAATAACTTGT
 TACAATAGGTTCTAAAATAAAATTGCTAACAGAAATGAAAATGGGAGATTGTAATTTACAACAGAAAAT
 TACCTTTGATTGTAACACTACTCTGCTGTTCAATCAAGAGTCTGGTAGATAAGAAAAAAATCAGTCATAT
 TTCCAATAATTGCAAAATAATGGCCAGTTGTTAGGAAGGCCTTAGGAAGGACAAATAACAAACAAACAG
 CCACAAATAACTTTTCTAAAATTGTTACCTGTAAATTATAAGAACTGATACAGACAAAACAGTTCC
 TTCAGATTCTACGGAATGACAGTATATCTCTTATCCTATGTGATTCTGCTCTGAATGCATTATTTCCA
 AACTATACCCATAAATTGTGACTAGTAAAATACACAGAGCAGAATTTCACAGATGCCAAAAAAATTAAA
 GATGTCAATATATGTGGAAAAGAGCTAACAGAGAGATCATTATTCTTAAAGATTGGCCATAACCTATATTT
 GATAGAATTAGATTGTTAAATACATGTATTCTACACATACTCTGTGTTAATAGAGACTTAAGCTGGATGTACTG
 CACTGGAGTAAGCAAGAAAATTGGGAAACTTTCTGTTGTTAGGTTGGCAACACATAGATCATATGTCTG
 AGGCACAAGTGGCTGTTCATTTGAAACCAGGGGATGCCAGCTAAATGAATATGCTGATGGGATTGCTAT
 CATAATATTACTATGCAGATGAATTCACTGAGGTCTGTGAGGTCTGTGCTCGTACTATCCTCAAATTATT
 TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTCAACAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
 TTCATTGCCCTCTATAAGCTCTGACTAGCCAATGGCATCATCCAATTCTCCCAAACCTCTGCAGCATCTG
 CTTATTGCCAAAGGGTAGTTCTGGTTCTGCAGCCATTGCGGTTAAAAATATAAGTAGGATAACTTGTAAA
 ACCTGCATATTGCTAATCTATAGACACCACAGTTCTAAATTCTTGAACCACTTACTACTTTTAAACTT
 AACTCAGTTCTAAATACCTTGCTGGAGCACAAAACAATAAAAGGTATCTTATAGTCGTACTTAAACTTTG
 TAGACCACAATTCACTTTAGTTCTTTACTTAAATCCCATCTGCAGTCTCAAATTAAAGTTCTCCAGTAG
 AGATTGAGTTGAGCCTGTATATCTATTAAAATTTCAACTTCCCACATATAATTACTAAGATGATTAAGACTTA
 CATTTCTGCCAGGCTGCAAAAACAAAATTATAAAACTAGTCCATCCAAGAACCAAGTTGTATAAACAGGT
 TGCTATAAGCTGTGAAATGAAACATTCAATCAAACATTCTCTATATAACAATTATTATTTACAAT
 TTGTTCTGCAATTCTTATGTCCACCCCTTAAAAATTATTATTTGAAGTAATTATTACAGGAAATG
 TTAATGAGATGTATTCTTATAGAGATATTCTTACAGAAAGCTTGTAGCAGAATATAATTGCACTATTGAC
 TTTGTAATTAGGAAAATGTATAAGATAAAATCTATTAAATTCTCCTCTAAACACTGAAAAA
 AAAA

FIGURE 42

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKRCHRDGMCCPSTRCNN
GICIPVTE SILTPHI PALDGTRHRDRN HGHYSNHD LGWQNL GRPHTKMSH IKGHEGD PCLRS
SDCIEGFCCARHF WTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAAATCCACCTACCTGGCCTCCAAA
 GTGTTGGGATTACAGGCCTGAGCCACCGCGCCGGCAACATCACGTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTCCTCCCTTAACCTCTATGTCAGAATGAGGAAGGA
 TAGCTGCATTTAGTCAGTTTCATTGCATAGTAATATTCATGTAGTATTTCTAAG
 TTATATTTAGTAATTCATATGTTAGATTAGGTTAACATACTTGAAAGAAACTTG
ATGTGTAAAGCCTTGGCAGAAATTCTGTATTGTTGAGGATTGTTCTTATCCCCCT
 TTTAAAGTCATCCGCTTGGCTCAGGATTGGAGAGCTGCACCACCAAAATGGCAAACA
 TCACCACTCCCAGATTGGACCAGTTGAAAGCTCCGAGTTGGCCAGTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCCCTACAACACTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTGACTCAAATCTCAACCTGAGCCATCCC
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGGCCAGGCAGTCAGTCACTGTTCTCCT
 CCTGGTTGGAGTCCTTCCCTCCAGGCAAAACTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTGCAGCTCCAGCAGCACCATTGAAAATATCTCTGTGCTG
 TCCACCAGCCACAGCCAAACACATCAAACATTGCTAACGGCGGATACCCCCAGCTCTAAG
 ATCCCAGCTCTGCAGTGGAAATGCCTGGTCAGCAGATGTCACAGGATTAAATGTGCAGTT
 TGGGGCTCTGGAATTGGGTCAAGAACCTCTCTGAATTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTGTATTGAAGTCTTAAGTGAGCCTTGAATACA
 TCTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTCCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACAAAGCCCTGTGAGTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGGGTGGTCAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTGTATGGCTGGGCCAACAAACAGAGGAAGAGGAGTAGTCACGTGA
 TGTGGAAAACACCAGTTGGTCAATGGCTCATTGCT**TAAA**AGCAGCCCTTGTCTTTGT
 TTTGGACCAGGTGGCTGTGGTTATTAGAAATGTCTTAACCACAGCAAGAAGGGAGGT
 GGTGGTCTCATATTCTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACTGATGCAT
 TTTAAAGATGCTTGGGCCAGGCAGGGTGGCTGATGCCATAATCCAGTGCTTGGGGGCC
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTGAGACCACCCCTGGCAACATGGTAAACTC
 TGTCTCTACTAAATACGAAAAACTAGCCGGGTGGTGGCGCGCGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPPLKSSVLGSGFGEAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSLNSASPAMSSSYDQSSVHNRIPYQSPVSSSESAP
GTIMNGHGGGRSQQTLDSKYSSKLLSWLVPTKQRKRIAHVMWKTPVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGCTGGCGGGGCC **ATG** GCGCTGCCATCCGAATCCTGCT
 TTGGAAACTTGTGCTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGCTGTACACCTGCAACCTGCACCCTCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGCACC CGCGCTTCTGACCTGCGTAACCGCGGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTAACAGGTGGTGCAC TGGGACCGGCAGCCGCCCGGG
 GTCCCGCACGACCGCGCGACCGCCTGCTGGACCTCTACGCGTCGGCGAGCGCCGCCCTA
 CGGGCCCCTTTCTGCGCGACCGCGTGGCTGTGGCGCGGATGCCTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCTTCCACCTGACGGTCGCCAACCCACGC
 GGAGCCGCCCGGGCTCTCCGGCAACGGCTCCAGCCACAGCGGCCAGGCCAG
 ACCCCACACTGGCGCGCGGCCACAACGTATCAATGTATCGTCCCCGAGAGCCGAGCCCAC
 TTCTCCAGCAGCTGGCTACGTGCTGCCACGCTGCTGCTTCTCATCCTGCTACTGGTCAC
 TGTCCCTGGCCGCCCGCAGGCGCCGGAGGCTACGAATAACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCCTGCCAAGTACATCGACCTAGACAAAGGGTCCCGAAGGAGAACT
 GCAAAT**AGG**GAGGCCCTGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGCATCTCCTGATGCTCCGGGCTCACCCCCCTCCAGCGGCTGGTCCCGCTTCC
 GGAATTGGCCTGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCCCTGGCTCACGGGTGCCCTGCCACCCCTGGCACACC
 AAAATCCCAC TGATGCCCATCATGCCCTCAGACCCCTCTGGCTCTGCCCGCTGGGGCCTG
 AAGACATTCTGGAGGACACTCCCACAGAACCTGGCAGCCCCAAA ACTGGGT CAGCCTCA
 GGGCAGGAGTCCCACCTCCAGGGCTCTGCTCGTCCGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCACAGAACCTGGCAGCCTGAAGTTGGGT CAGCCTCGGCAGGAGTCCCAC
 CCTCCTGGGTGCTGCCACCAAGAGCTCCCCACCTGTACCAACCATGTGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTGAATGCCAGCCCTGCTCCTGTGTTG
 CTTGGGCCACCTGGGCTGCCACCCCTGCCCTTCTGCCCATCCCTACCCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCAGTGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCC
 GGACTCTGCCCTGGGCTGGAGTCTAGGGCTGGGCTACATTGGCTTCTGACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTGGGTGCCCTGTGTTGCCACTCTCAGCACCCACATT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAGTCCCCATCTGATTTAAAAAAAAAA
 AAAAAA

FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLA VARGAPALLTCVNRGHVWTDRHVEEAQQVVHWRQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADA FERGDFSLRIE PLEVADEGTYSCHLHHHYCGLHERRVF
HLTV AEPHA EPPP RGS PGNG SSG HSGA PGDP TLARGHN VINVIVPESRAHFF QQLGYVLATL
LLFILLLV TILLAARRRRGGYE YSDQ KSGK SKGD VN LAEFAVAAGDQML YRS EDI QLDYKN
NILKERAELAH SPLPAKYIDL DKGFRK ENCK
```

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGCGTGGCGCAGGGCAGCAGCTGTCTCAGAGGACGACTTT
 CAGCACAGTTCAAACCTCACCGAACACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCGCCCCCTGGCTGCAGAGGCCAGGGACCGCTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGCATTGGCAGTCACTGCCATGGAACCTCTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCGCAACTCCTCCAGCCCAGCCACCGGGGA
 GGACCCGTAGGGCTCAGACATCCTGAACACTTTGAGAGCTACCTTGCCGTTGCCCTCACCG
 TGCCCTCCATGCTGCTGGCCAACCTCTGCTTGTCAACAGGGTTGCAGTCCACATC
 CGTGTCCCTGGCCTCACTGACGGTCATCCTGGCATCTTATGGTATAACTGCAGTGGTAA
 GGTGGACACTTCCCTGGACCCGTGGTTTTTGCGGTCACCATTGTCTGCATGGTATCC
 TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTCTATG
 AGGAACCTCCAAGCAGCACTGATATCAGGAGGGACATGGGGGACGGTCAGGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGTGAGGAACAGCGCCCTGGCCTCTTCCGTACGG
 CCACCATCTCCTCGTCTGCATGGACTCTACCTGCTGCTGCCAGGCTGGAGTATGCC
 AGGTAACATGAGGCCTGTTCTGGCCCATGTGTTCTGGTAAGAGGAGCTCCCCA
 GGACTCCCTCAGTGCCTTCGGTGGCCTCCAGATTGATTCCCACACACCCCCCTCTCC
 GCCCCATCCTGAAGAAGACGCCAGCCTGGCTCTGTGTCACCTACGTCTTCTCATCACC
 AGCCTCATCACCCCGTCTGCACCAACATCGAGTCCTCAACAAGGGCTGGGCTCACT
 GTGGACCACCAAGTTTCATCCCCCTCACTACCTTCTGTACAACATTGCTGACCTAT
 GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCAACAGCAAGGCCTCCAGGG
 TTCGTGCTCCTGGGACCTGCCTCATCCCCCTTCTGCTGTAACTACCAAGCCCCCGGT
 CCACCTGAAGACTGTGGCTTCCAGTCGATGTGTAACCCGCACCTCAGCTCCGTGG
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCTACGGGCTAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGTGCTTTATGTGTGCTGGGCTAACACTGGG
 CTCAGCCTGCTCACCTCTGGTCACCTCATC**TAGAAGGGAGGACACAAGGACATTGGT**
 CTTCAGAGCCTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC
 TAAAGTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCAAAGATGCCA
 GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAAAGAACACT
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGTACTCCCTCACAGCTGATGGTTA
 ACATTCCACCTTCTTAGCCCTCAAAGATGCTGCCAGTGTGCTGCCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCCTTACCTGAAGGGTCTCCCTGGAATGGA
 AGTCCCCTGGCATGGTCAGTCCTCAGGCCAAGACTCAAGTGTGACAGACCCCTGTGTTCT
 GCAGGGTGAACAACTGCCACTAACAGAGCTGGAAAACCCAGAAAGATGGGCTTCCATGAAT
 GCTTCATTCCAGAGGGACCAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
 TTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGCTAAGATGAGGGTC
 TTTCAGTGTCCCTGTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAAACTTGC
 GTATTCAAAA

FIGURE 48

MAVVSEDDFQHSSNSTYGTTS defense protein
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
LVNRVAHVIRVLASLTVELAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
LLLCSRLEYARYYMMPVLAHVFSGEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLG
CVTYVFFITSЛИYPAVCTNIESLNKGSGSLWTTKFFIPLTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTACCAAGAGCTGGAGACACCA
 TCTCCCACCGAGAGTC**ATG**CCCCATTGGCCCTGCACCTCCTCGCCTCGTCCCCATCCTCC
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTAACGCAGCCAAGACCCCTCGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTACCTGGGGCTCAATCGGACCT
 GAAGCCCCAGAGGGTGAATTGGTTGGCGCTGGTGTGCCGGCTGGTGGCCGCCAAGGTGC
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATGGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGAGCTGGGAGCCATGCGCATGCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGCTCAACCTGACCAAGTTACCC
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCCGAGAAGCTGGCTACGCCCTGCGTCCCCAGGAAAAGGCCACTGCCCGAAGA
 CATCTACCAAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCAGTGGCTGCAGAAAGG
 CGATGAAGAAGTTGAAAGGCACACGCTTGGAAATATCTCTGGGGAGGGAACCTGAGC
 CGGCCGGCCGTGCAGCTCTGGAGACGTGATGTCCGAGGATGGCTTCTATCTCAGCTT
 CGCCGAGGCCCTCCGGGCCACAGCTGCCCTAGCGACAGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGACCTGCTGCCGCGCGCTGCTGAGCTCGCTGTCCGGCTTGCTGTTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCACGTGGTGTGCTGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTCTGCCGCCGCTGCCCGCACATGCAGGAGGCAGTGCAGGAGG
 CTGCACTACGTGCCGCCACCAAGGTGTTCTAACGCTTCCGAGGCCCTCTGGCGCGAGGA
 GCACATTGAAGGCCACTCAAACACCGATGCCCGTGCATGATTTCTACCCGCCGC
 CGCGCAGGGCGCGCTGCTGGCTCGTACACGTGGTGGACGCCGGCAGCGTGGCG
 GGCTTGAGCCGGGAAGAGGCAGTGGCTGGCGCTCGACGACGTGGCGGATTGCACGGCC
 TGTCGTGCCAGCTCTGGACGGCACCGCGTGTCAAGCGTTGGCGGAGGACCGACA
 GCCAGGGTGGCTTGTTGTTGACAGCCGCCGGCCTCTGGCAAACCGAAAAGGATGACTGGACG
 GTCCCTTATGGCCGCATCTACTTGCAGGGCGAGCACACCGCTACCGCACGGCTGGGTGGA
 GACGGCGGTCAAGTCGGCGCTGCGCGCCATCAAGATCAACAGCCGAAGGGCCTGCAT
 CGGACACGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGCAGGGCATGTGCATGG
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG
 CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTCGGAAAAA
 AA

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKPEKLGYALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFYLSFAEALR
AHSCSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVVLITASGPRAVKRITFSPPPLRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTS

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGCCTTCTGCCTGC**AT**
GGACGCTCTGAAGCCACCCCTGTCTGGAGGAACCACGAGCGAGGGAAAGAAGGGACAGGGACTCGTGCGCAGGAA
 GAACTCAGAGCCGGGAAGCCCCCATTCACTAGAACGACTGAGAGATCGGGCCCCCTCGCAGGGCTGAATTTCCT
 GCTGCTGTTCACAAAGATGCTTTTATCTTAACTTTGTTTCCCCACTTCCGACCCCGCGTTGATCTGCAT
 CCTGACATTTGGAGCTGCCATCTTCTGTGGCTGATCACCAGACCTCAACCCGCTTACCTCTTGACCTGAA
 CAATCAGTGTGGAAATTGAGGGAGGAGCACGGAAGGGGTTCCAGAAGAACAAATGACCTAACAGTTGCTG
 CTTCTCAGATGCCAACAGACTATGTATGAGGTTTCAAAGAGGACTCGCTGTCTGACAATGGGCCCTGCTGG
 ATATAGAAAACCAAACAGCCCTACAGATGGCTATCTTACAAACAGGTGCTGATAGAGCAGAGTACCTGGGTT
 CTGTCCTTGATCAAAGGTTATAAATCATCACCAGACAGTTGTCGGCATCTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCGAATTGGCTGTTACACGTACTCTATGGTAGCTGTACCTCTGATGACACCTTGGGACCAGAAC
 CATCGTACATATTGTCAACAAGGCTGATATGCCATGGTGTCTGACACACCCAAAAGGCATTGGTGTGAT
 AGGGAATGTAGAGAAAGGCTTCACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTGATGATGACCTGAA
 GCAAAGAGGGAGAAGAGTGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGAAAGAGCACTTCAG
 AAAACCTGTGCCCTCTAGCCCAGAACGACTGAGCGTCATCTGCTTACCCAGTGGGACCACAGGTGACCCAAAGG
 AGCCATGATAACCCATCAAATATTGTTCAAATGCTGTCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCCTGATGATGTCGGCATATCCTACCTCCCTGTCATATGTTGAGAGGATTGTACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGAGTTGATTCTCCAAGGGGATATCGGTTGCTGGCTGACGACATGAAGACTTGAAGCC
 CACATTGTTCCCGCGGTGCTCGACTCCTAACAGGACTACGATAAGGTACAAATGAGGCAAGACACCCCT
 GAAGAAGTTCTGTTGAAGCTGGCTGTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGGTTGTAATTGTCAGTGGGAC
 TGCCCCCATGTCCACTTCAGTCAGTCATGACATTCTCCGGGAGCAATGGGATGTCAGGTGTTGAAAGCTTATGGTCA
 AACAGAATGCCACAGGTGGCTGACATTACATTACCTGGGACTGGACATCAGGTACACGTTGGGGTCCCCGG
 TTGCAATTACCGTGAAGCTGGAGATGTGGCTGACATGAACACTTTACAGTGAATAATGAAGGAGAGGTCTGCA
 CAAGGGTACAAACGTGTCAAAGGATACCTGAGGGACCTGAGAACACAGGAAGGCCCTGGACAGTGTGGCTG
 GCTTCACACAGGAGACATTGGTCGCTGGCTCCCAGAACGAACTCTGAAGAGTCATCGACCGTAAAAAGAACATT
 CAAGCTGGCCAAGGAGAACATATTGACACCAGAGAACGAAAGATGAAAGATGAAAGAACAGGAGTCACCCAGTGT
 AATTTTGACACGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTTCTGACACAGATGACTTCCCTC
 ATTGCAAGCTTGGGTGAAGGGCTCCTTGAGGAACGTTGCAAAACCAAGTTGTAAGGGAGGCCATT
 AGAAGACTTGCAAGAAAATTGGGAAAGAAAGTGGCCTTAAACTTTGAACAGGTCAAAGCCATTTCATCC
 AGAGCCATTTCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCAGGAGAGCTTCAAATACTT
 TCGGACCCAAATTGACAGCCTGATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGCCACTG
 TGCACGTGTTGAGAAAATGGATTAAAATCTTACATTGTTGCCTTCCCTTATTTTTTAACC
 TGTAAACTCTAAAGCCATAGCTTGTATATTGAGACATATAATGTGAAACTTAGTCCAAATAATCA
 ATCCGTCTTCCATCTCGATGTTGCTAATATTAAGGCTCAGGGCTACTTTATCAACATGCCTGTCTCAA
 GATCCCAGTTATGTTCTGTGCTCTCATGATTCCAACCTTAATACTATTAGTAACCACAAGTCAAGGGT
 CAAAGGGACCCCTGTGCCCTCTTGTGATAAACATAACTGCCAACAGTCTATGCTTATTTACA
 TCTCTACTGTTCAAACATAAGAGATTTAAATTCTGAAAAACTGCTTACAATTCACTGTTCTAGCCACTCCAC
 AAACCACTAAATTTAGTTAGCCTATCACTCATGTCATCATATCTATGAGAACAAATGTCTCCGATGCTCTT
 CTGCGTAAATTAAATTGTTGACTGAGGGAAAAGTTGATCATACCCAAACATTCTCAAACCTCTAGTTAGATA
 TCTGACTTGGGAGTATTAATTGGGTCTATGACATACTGTCACAGGAATGCTGTTCAAAGCATTATT
 CAGTAGGAACCTGGGAGTAAATCTGTTCCCTACAGTTGCTGAGCTGGAGCTGTGGGGAGGGAGTTGACA
 GGTGGGGCCAGTGAACCTTCCAGTAAATGAAGCAAGCAACTGAATAAAACCTCCTGAACACTGGGAACAAAGATCT
 ACAGGCAAGCAAGATGCCACACAAACAGGCTTATTCTGTGAAGGAACCAACTGATCTCCCCACCCCTGGATT
 AGAGTTCTGCTCACCTTACCCACAGATAACACATGTTGTTCTACTGTAAAGTCTTAAAGTCTTAAAC
 TATTACAGATAAAAAAA

FIGURE 52

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFQAQNRPWEWIISELACYTYSMVAPELYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSSLKVIIILMDPFDDDLKQRGEGKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAAFLKCVEHAYEPTPDDVAISYLPalahMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKELOKGIIRHDSFWDKLIFAKIQDSLGGRVRVIVTGAAPMSTSVMFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHGVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLGVVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVRALLEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLPTLKAKRGELSKYFRTQIDSILYEHIQD
```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGC GGAGGCC CGGGCGAGCCGGCCGAGCAGTGAGGGCCCTAGCGGGGCCAGCGGGGG
 CCCGGGGCCCTAAGCCATT CCTGAAGTCATGGCTGGCCAGGACATTGGTACCCGCCAAT
 CCGGT**ATG**GACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTGGGCTCGGAAGAACGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCAGGAGATTCTGTCA
 GACAGGGCCGTGCTTCTGCTGGTACTGTCAATTGTCAATATCAAGTTGATCCTGGACA
 CTAGGCCGAGCCATCAGTAAGCCAATGAAGACCCAGAGGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCACGGCGCAGAGGCCAGTGGTCCCCGGCTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACTGGTGTGGAGGATG
 AGGCCGGGAGCAGGGCCGGGCATCCATGTCAATTGTCTCAACCAGGCCACGGCCACGTG
 ATGGCAAAACGTGTGTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGTATTCT
 CAACATGGTAGCGCCCGGGAGTGCTCATCTGCACTGTCAAGGATGAGGCCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGCAGCCAGGCTGCCCTGCCCTGGC
 TGGAGGGACACATGGGCTTCTGGAGCAGAAAAGGAGGTCTGTCTCGGGAGAACATTC
 TAAGTCACCTGCCCTCTTCTGGGGGACCCAGTCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTGCACACTGGCAGACACAGAGCTGAACCGTCGCCGGCGC
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCATCGA
 GTTCAGCCCTGACCCACTCCCAGACAAACAAGGTCTCAATGTGCTGTGGCTGTATTGCAG
 GGAACCGACCCATTACCTGTACAGGATGCTGCCTCTGCTTCAAGCCCAGGGGTGTCT
 CCTCAGATGATAACAGTTTCAATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
 GTTGGTCTGAGGGCATCCAGCATACTCCATCAGCATCAAGAATGCCCGTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTCAGTTCTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTGCCTGGAATGACCAGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGCTGGCTGGGTGCTC
 AGGAGGTCTGTACAAGGAGGAGCTTGAGCCCAAGTGGCTACACGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGCGAGAGTGCATCATCCCTGACG
 TTTCCGATCCTACCACTTGGCATCGTCGGCTCAACATGAATGGCTACTTCAAGGAGGCC
 TACTTCAGAAGCACAAGTTCAACACGGTCCAGGTGCTCAGCTAGGAATGTGGACAGTCT
 GAAGAAAGAAGCTTATGAAGTGGAGTTCACAGGCTGCTCAGTGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCCTGTGAAGACTCTTCCCTGCCAGACACAGAGGCCACACCTACGTGGCC
 TTTATCGAATGGAGAAAGATGATGACTCACCACCTGGACCCAGCTGCAAGTGCCTCCA
 TATCTGGGACCTGGATGTGCGTGGCAACCCTGGGGCTGTGGAGATTGTTGGAAAGAAGA
 ACCACTCCCTGGTGGTGGGGTCCCGGCTCCCCCTACTCAGTGAAGAACGCCACCCCTAGTC
 ACCCCAAATTCTGGAGCCACCCCCAAGGAGGAGGGAGGCCAGGAGGCCAGAACAGAC
ATGAACCTCCTCCAGGACCCCTGCAGGGCTGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTGAGATGCTGGTAGGGCTGGGCTACCTTGTGTTTAACA
 TGAGACTTAATTACTAACCAAGGGAGGGTCCCTGCTCCAACACCCGTTCTGAGTT
 AAAAGTCTATTATTACTTCCCTGTTGGAGAAGGGCAGGAGAGTACCTGGAAATCATTACG
 ATCCCTAGCAGCTCATCCTGCCCTTGAATACCCCTACTTCCAGGCCTGGCTCAGAATCTA
 ACCTATTATTGACTGTGCTGAGGGCCTGGAAAACAGGCCGAACCTGGAGGGCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTTACTCAGGAAACTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCTA
 GACACTGGGACCCAGGCCCTCTCAGCCTCTTGTCCAGATTCAAAGCTGGATAAGTT
 GGTCAATTGATTAAGGAGAAGGCCCTGGGAAAAA

FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
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REQGRGIHVIVLNQATGHVMAKRVFDTYSPEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGPPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRLRFCSKVEGYGSVCSCDKPTPIEFSPDPLPDNKVLNPVAVIAGN
RPNLYRMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSDLKKEAYEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDL DVRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
```

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGGTGGGAAGGCCTAAAGAACGGAAACTGGAAAGCCCACCTCTCTTGGAACCCACAC
 CTGTTAAAGAACCTAACGACCATTAAAGCCACTGGAAATTGTTGTAGTGGTTGTGGATGTTA
 AAGGAGGGCAGA**ATG**GATTTCATCTCATTAGCCTGCTGTCTGGCTATGTGGTGGATGTTA
 CGTGGCCGGAATCATTCCCTGGCTGTTAATTCTCAGAGGAACGACTGAAGCTGGTACTGTTGG
 GTGCTGGCCTCTGTGGAACTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTATGAA
 GATATTCTTGAGGGAAAACACCAAGCAACTGAAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCCACACAGCTGCATGCCTATATTGGTG
 TTTCCCTCGTTCTGGGCTCGTTTATGTTGCTGGTGGACCAGATTGTAACCTCCATGTGCATTCT
 ACTGACGATCCAGAACAGCAGCAAGGTCTAGCAATTCCAAAATCACCACACGCTGGGCTGGGTGTC
 TGCTGCAGCTGATGGTGTGCTTGGAGCAGCAGCATCTACCTCACAGACAGCAGTGTCCAGTTAATTG
 TGTTGTGGCAATCATGCTACATAAGGCACCAAGCTGCTTTGGACTGGTTCTTCTTGATGCATGCT
 GGCTTAGAGCGGAATCGAATCAGAAAGCAGCTGCTGGTCTTGCATTGGCAGCACAGTTATGTC
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAACGCCCTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTCTGCCCCGACATTCTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGCGGA
 ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCTGGAAAGTGGCAGCC
 GGTCTGGGTTGCCTCATCCCTCATCCTGTCAGTAGGACACCAGCATTAA**TAA**ATGTTCAAGGTCCAGC
 CTTGGTCCAGGGCCGTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTCCTCAGTC
 TCTGTCTCACCTGCGCATCTACATGTATTCTAGAGTCAGAGGGAGGTGAGGTAAAACCTG
 AGTAATGGAAAAGCTTTAGAGTAGAAACACATTACGTTGAGCTAGTATAGACATCCATTGTGT
 TATCTTTAAAAGGCCCTGACATTGCGTTAATATTCTCTTAACCTATTCTCAGGGAAAGATG
 GAATTAGTTAAGGGAAAAGAGGAGAACCTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGTCCTTCTTAGTTAGAGGCCTGCTACTTATCCATTGATTTT
 AACATGGTCCCACCATGTAAGACTGGTCTTAGCATCTATGCCACATGCGTTGATGGAAGGTATA
 GCACCCACTCACTTAGATGCTAAAGGTATTCTAGTTAATCTGGATTAGGGTCAGGAAAATGATAGC
 AAGACACATTGAAAGCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT
 TAAACAGCTCCTTGGCACGTGCCCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG
 TGGGAGGAGCTCTAAAGAGGTGACTGGTATTGTCAGTCTAGTTAGGCTTCTCAGTCTAGGCTTCTCAAGAA
 CAGTCAGATCACAAAGTCTTGGAAATTAGGGATATTAAATTAAAGTGTATTGGATGGTTAT
 TGATATCTTGTAGCTTTTAAAGACTACAAAATGTATGGTGTCTTTTTGGTTTT
 TTTTTTTAATTATTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAAGCTT
 GGCGACACTGTGTCCTCACATAACCACCTGTAGCAAGATGGATCATAAAATGAGAAGTGTGCT
 TTGATTAAAGCTTATGGATCATGTCCTCTCGTCTTGTCTCTCGTCTTTCTGCTTTCTCAACTTT
 TCCCTCTAGCCTCTCCGCCACAATTGCTGCTACTGCTGGTGTAAATTGTTGTCAGGCTTCT
 CTTATCAGGACAACCACTCTCGAACTGTAATAATGAAGATAATAATCTTATTCTTATCCC
 CAAAGAAAATTACCTTGTGTCAAATGCCGCTTGTGAGGCCCTAAACACCCCTCATGTGAA
 ATTGACACAATCACTAATCTGGTAAATTAAACAATTGAGATAGCAGAAAAGTGTAAACAGACTAGGATA
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 TATAATTATTATTACTTCTATACCATTTCAAAACACATTACACTAAGGGGGAACCAAGACTAGTT
 TCTCAGGGCAGTGGACGTAGTAGTTGTAACCTGTTCTATGACGCTAGCATGCCTATG
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 GGCCACAGTGGAGGAAAGTAGCAGCAAAATAGGATACAGTTGTATGTCAGTCTGGCAACAATTG
 ATTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTCCCTGATTGGATGTTAACAGCT
 GACTGGTGTGAGACTTGAGGTTCATCTAGCCTTCAAAACTATATGGTGCCTAGATTCTCTGGA
 AACTGACTTTGTCAAATAAGCAGATTGTAGTGTCAAAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVVDQ
IGNSHVHSTDDPEAARSSNSKITTLGLVVHAAADGVALGAAASTSQTSQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGCGGCCTCGTAGCGGGGCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTGAG**ATG**ATGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCCTGGCCCTGGTGGCCTGCATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCGGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAACGAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTCCAGCTGGAGAGCGTCAACAGCTGTACCAGGACGAAAAGGGGTTTGGTGAA
 TAACATCACCACAGGTGAGAGGGCTCATCCGAGTGCTGCAAGACCAGTTAAGACCCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTCAAAGAACAGACCAACCTGGAG
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGGCCAGGCTGCAG
 GCAGCAGGCCCTGCCACACACAGAGGTGCCACAAGGGAAACGTGCTGGTAACAGCAA
 GTCCCCAGACACCAGCCCCCAGTCCGAAGTGGTTGGATTCAAAGAGACAAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGGTGGTAATGAGGAGCCTCAGAGGGACAGGCTGCCAGGAG
 CCAGGCCGGAGCAGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTGGAGGCCGG
 AGAACTGGGCCAGACCCCCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTGTCACTCCCGACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGAAGGGAGAAACCAGCAGAAACTGAGAGGAGAAGATGACTACACATGGATGAAAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGATGACAGAAACATAGATG
 TTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTACTTGATCAGCGTGAAAAGCGG
 AATCATAACACTC**TGA**ATTGAACTGGAATCACATATTCACAACAGGGCGAAGAGATGACTA
 TAAAATGTTCATGAGGGACTGAATACTGAAAATGTACTAAATAATGTACATCTGA

FIGURE 58

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAERGA
VELKKNEFQGELEKQREQLDKIQSNSHNFQLESVNKLQYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNNDQRQQQLQALSEPQPRLQAAGLPHTEVPGKGNVLGNSKSQTPAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEPMREQVVEDRPVGGRGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFVNVEDQKRDTINLLDQREKRNH

Signal peptide:

amino acids 1-29

FIGURE 59

GGATGCAGAAAGCCTCAGTGGCTCTTCCTGGCCTGGGTCTGCTTCCCTTCTACGCTGGCATTGCCCTTTCA
 CCAGTGGCTTCCCTGCTCACCGTTGGAGCTCACCAACCATAAGCAGCTGCCAAGAGCCCCCAGGCCCTGGTCCC
 TGCATGGGGAGCCAAGGGAAACCTGGGCCCTGCTGGATGGCTCCCGATTTCGGGGTTGTGTTGGTGTGA
 TAGATGCTCTGCGATTGACTTCGCCAGCCCCAGCATTCACACGTGCCCTAGAGAGCCTCTGTCTCCCTACCCCT
 TCCTGGGCAAACTAAGCTCCTTGAGAGATCCTGGAGATTCAAGCCCCACCATGCCCGCTCACCGATCTCAGG
 TTGACCCCTCCTACCACCAACCATGCAGGCCCTCAAGGCCCTACCACGGTCACTGCCAACCTTATTGATGCTG
 GTAGTAACCTGCCAGCCACGCCATAGGAAAGACAATCTCATTAAGCAGCTCACCAAGTGCAGGAAGCGTAG
 TCTTCATGGGAGATGATACTGAAAGACCTTTCCCTGGTCTTCTCAAAGCTTCTTCCCATCCTTCA
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGAAACACCTAACCCACCATGGACAGTGGTGAATGGG
 ACAGTGTGATTGCTCACTCCTGGGTGTGGACCACTGTGCCACAAGCATGCCCTACCACCCGAAATGCCA
 AGAAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAAATGACACACTGCTGGTAGTGG
 CTGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGACAGTGAGCTGGAGGTCTAGCTGCTCTTT
 TGTATAGCCCCACAGCAGCTTCCCCAGCACCCACCAGAGGGACAGGGTGAATTCTCAAGTTAGCCTTG
 CCACGCTGGCCCTGCTGGCCTGCCATCCATTGGGAATATGGGGAAAGTGTGGTGAAGCTATTCTCAG
 GGGTGGAGGACTCCCAGCCCCACTCCTCTGCTTAGCCCAAGCCTCAGCTCTCATCAATGCTCAGCAGGTGT
 CCCGATTCTTCATACCTACTCAGCTGCTACTCAGGACCTCAAGCTAAGGAGCTCATCAGCTGCAGAACCTCT
 TCTCCAAGGCCCTGCTGACTACCAGTGGCTTCTCCAGAGCCCAAGGGGCTGAGGCAGACTGCCACTGTGA
 TTGCTGAGCTGAGCAGTCAGTCCCTGCGGGGAGCTGGGCATGTGCATCGAGTCTGGCTCGTTCTCTGGTCC
 GCATGGCGGGGGTACTGCTCTTGGCTGCTCCTGCTTATCTGCTGCTGCATCTCAGTGGCAATATCCC
 CAGGCTTCCATTCTGCCCTACTCCTGACACCTGTGGCTGGGCTGGTTGGGCCATAGCGTATGCTGGAC
 TCCTGGGAAACTATTGAGCTGAAGCTAGATCTAGTGCTTAGGGCTGTGGCTGAGCTGAGCTCATTCTCC
 TTCTGTGGAAAGCCTGGCTGGCTGGGCTGGCAAGAGGCCCTGGCAACCCCTGGTCCATCCCTGGCCCCGTCC
 TGTTACTCCTGCTGTTGCTGGCTGTTCTCTGATAGTTGTTAGCTGAGGCCAGGGCAGGGCACCCCT
 TCCCTTGGGCTCATTCCTGCTCTGGTGTGAGCTTCAAGGCTACTGGAGGGCAGCTGCTTCCACCTAAC
 TCACAATGCCCGCCCTGGCACTTCAGCCACAACAAACCCCCACGGCACAAATGGTCATATGCCCTGAGGCTTG
 GAATTGGGTTGCTTTATGTACAAGGCTAGCTGGCTTTTCACTGGTGGGTGGCTGAGCCAAGAATT
 TGTTAGCTGAGGCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
 CGCGCTGGGGCCCTGGTAGCTGCCGTGCGCTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
 CCATGCTTTGTGCGCTGGGACTGCCCTAATGGCATGGTACTGCTGCCACTGGCATTGGCTGGGG
 CAGATGAGGCTCCCCCGCTCCGGGCTCTGGGTCTGGCTCTGGGCTGGCTGGCTGGCTGGCTGG
 TGGCTGCTTCAGGGCTCCGCTGCTGCTGGAGGCTGTGACAGTGTGGTGAAGGCTGGGAGGGCTCC
 GGACAGGACTGCTCTCAGGCCCTCTCAGGCCCTCAAGCTGACTGGATTATGTGGCCCTCAA
 TCTACCGACACATGCAGGAGGAGTCCGGGGCGGTTAGAGAGGACAAATCTCAGGGCTCCCTGACTGTGGCTG
 CTTATCAGTTGGGAGTGTCTACTCAGCTGCTATGGTCAGGCCCTCACCCCTGGCTTCCACTCTGCTGT
 TGCATGCGAGCGCATCAGCCTGTGTTCTGCTTCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
 CTGGGATACCGTCACCACCCCTGGCTTACTGTGCCATGGCAGGCAGTCTGGCTGGGCCCTCATGCCA
 CACAGACCTACTCCACAGGCCACCAGCCTGCTTCCAGGCCATCCATGGCATGCGAGCTTCCGGTGGGATTCC
 CAGAGGGTCATGGCTCTGTACTTGGCTGCCCTGGCTAGTGGAGGCAACACCTTGGCTCCACCTCT
 TTGAGCTAGGGTGGCCACTGCTCTGCTGGCTTCTGCTGGAGAGTCAGGGCTGGGAAGAGACAGCAGC
 CCCAGGGAAAGCTGATGCCAGAGTCAGACCCGAGGGAGAAGAGGAGGCCACTGATGGAGATGCGGCTCC
 ATGCCCTCAGCAGCAGTGTGGAGAACAGTGTAGCCTGGCAGTGGCTGGCTGGCTGGCTGG
 TGGCTGTGCCCTGGCAGCCTCCATCCTCGAGGCATCTCATGGCTGGAAAGTGTGTTGCCCTAAGTT
 TTGAGGCTGTGGCTCAGGCAGCTATTCTGGCCAGCAGAGG**TAG**CCTAGTCTGTGATTACTGGCA
 TCTACTATCATGCAGCCAGGGCCGCTGACATCTAGGACTTCATTATCTATAATT
 TGATCCCTAAGCTCTGATTGGATGCATCTGAGGGACAAGGGGGGGGGCTCCGAAGTGGAAATAA
 AGGCCGGCGTGGTAGCTGCACCTATAATCCAGCACTTGGGAGGCAGAGGTGGGAGGATTGCTGG
 AGACCCGAGTGAATAAAAGTGAATAAAATGATAATAT

FIGURE 60

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
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MASRFSRVVLVLIDALRFDAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTMQRALKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLF
PGAFSKAFFFPSFNVRDLDVTNGILEHLYPTMDSGEWDVLIAHFLGVDHCGKHGPHEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIFGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRLFHTYSAATQDLQAKEHLQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGFPFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAYVSSFLPFLWKAWAGWGSKRPLATLFPPIPgpVLLLLFRLA
VFFSDSFVVAEARATPFLLGSFILLLVQLHWEGQLLPPKLLTMPLRGTATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
RAVAGLAASGLALLIWKPVTVLVKAGAGAPRTRTLTFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAAYQLGSVYSAAMVTALTLLAFPLLLHAERISLVFLLLFQSFL
LLHLLAAGIPVTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVPAIHWHAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKRQQPPGNEADARVRPEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFIQIQLACALAASILRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLGIALVMRVDGAVSSWFRQLFLAQQR
```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCGGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGGACGGGCAGTCCCTGT
 GTCTCTGGGTTGCCTAACACCTGCAAACATCACCTCTTATCCATCAACATGAAGA**ATGT**
 CCTACAATGGACTCCACCAGAGGGTCTCAAGGAGTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGT
 CCTGACAGCTCCAGAGAAGTGGAAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGTCACCTGGCTGGAGCCGAACACTCTTACTGCGT
 ACACGTGGAGTCCTCGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTG
 CCAGGACTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTCTGGTATGTTTG
 CCCATATCTATTACCGTGTCTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAATTGATTGATTGAAATGAATTGACAAAAA
 GATTCTTGTGCCTGCTGAAAAAATCGTGATTAACTTATCACCCCTCAATATCTGGATGAT
 TCTAAAATTCTCATCAGGATATGAGTTACTGGAAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
 GGTATGCTTCGCATTGATGAAATTGGACTCTGAAGAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAACCCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTGTCGGGGCCTGAAGAGCAGGAGCTCAGTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTGGAGTCGCAGGCAGCGTTGGCAGTCTGGGCCCG
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCAGTGGATCCCC
 AAACTGGCAGGCTGTATTCCCTCGCTGTCCAGCTCGACCAGGATTCAAGGGCTGCGAG
 CCTCTGAGGGGGATGGGCTCGAGAGGGAGGTCTATCTAGACTCTAGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCACTGGAGGAATGGGGT
 TATATGTGCAGATGAAAC**TGA**TGCCAACACTCCTTGCCTTGTGCAAAC
 AAGTGAGTCACCCCTTGATCCCAGCCATAAAGTACCTGGATGAAAGAAGTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTG
 GTTCATGCATGTAGGTCTCTAACATGATGGTGGCCTCTGGAGTCCAGGGCTGGCCGGT
 TGTTCTATGCAGAGAAAGCAGTCATAAAATGTTGCCAGACTGGGTGCAGAATTTCAGG
 TGGGTGT

FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCISISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSLNTKSRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQ
CARTLKQDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDF
KRFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAALAVLGPQLQSYTPQLQDLDPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDGGLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQmen
```

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGTCTCTGCAGGGAGACGCCAGCCTGCG
 TCTGCC**ATG**GGGCTCGGGTTGAGGGCTGGGACGTCCCTGCTGACTGTGGCCACGCCCT
 GATGCTGCCGTGAAGCCCCCGCAGGCTCCTGGGGGCCAGATCATCGGGGCCACGAGG
 TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGCCAACATCACTGCGGA
 GGCTTCCTGCTGCGAGCCCCTGGGTGGTCTCGGCCGCCACTGCTTCAGCCACAGAGACCT
 CCGCACTGGCCTGGTGGTGCTGGCGCCACGTCCTGAGTACTGCGGAGCCCACCCAGCAGG
 TGTTTGGCATCGATGCTCTCACACGCACCCGACTACCACCCATGACCCACGCCAACGAC
 ATCTGCCTGCTGCGCTGAACGGCTTGCTGTCCCTGGGCCCTGCAGTGGGCTGCTGAGGCT
 GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGACACGGTGCCGGTGGCTGGCTGGGCT
 TCGTGTCTGACTTGAGGAGCTGCCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
 CCGGACGTCTGCAACAGCTCCTGGAAGGGCACCTGACACTTACCATGCTCTGCACCCGCA
 TGGGACAGCCACAGACGGGCTTCTGCTCGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
 ACCGGGCTCACGGCCTCGTTCTCGGGCCTCTGGTGCAGGCCACCCAAAGACCCCGAC
 GTGTACACGCAGGTGTCGCCTTGTGGCCTGGATCTGGACGTGGTTCGGCGAGCAGTCC
 CCAGCCCCGGCCCTGCCTGGACCACCAAGGCCCCAGGAGAACCGCC**TGA**GCCACAACCT
 TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
 AAGCCTGATGTTCAGGGTTGGGTGGGACGGGAGCGGTGGGCACACCCATTCCACATGCA
 AAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGACAAAAAAAAAAAAAGAAA

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSAETQQVFGIDALTTHPDYHPMTHANDIC
LLRLNNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLMCTRSGDHSRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCACTCCGGACGCCCTGACGCCCTGA
 CGCCTGTCCCCGGCCCGC**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGACGGTAG
 CAGGCGCCGCCGTGCTGCTCAAGGACTATGTACCCGGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTGACGGGCACACAGGCATGGGAAGCAGACCGCCTT
 GGAACCTGCCAGGAGAGGAGGAAACATCATCCTGCCCTGCCAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGGGGAGACCCCTCAATCACCATGTCAACGCCGGCACCTGGAC
 TTGGCTCCCTCAAGTCTATCCGAGAGTTGCAGCAAAGATCATGAAGAGGAGGAGCGAGT
 GGACATTCTAACAAACGCGGGTGTGATGCGGTGCCCTACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTGGCGTTAACCAACCTGGGTCACTTCTCTTGACAAACTTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCTCGCGGATCATCAACCTCTCGTCCCTGCCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAACACTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTGCCATCGCCTTCAACCAAGGAGCTGAGCCGGCGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGCAGACACACGGG
 CATCCATGGCTCCACCTCTCCAGCACCACACTCGGGCCCATCTCTGGCTGGTCAAGA
 GCCCGAGCTGGCGCCCAGCCAGCACATACCTGGCGTGGCGAGGAAGTGGCGGATGTT
 TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCCGGCCCCGAGGCTGAGGATGAGGA
 GGTGGCCCGGAGGCTTGGCTGAAAGTGCCGCCTGGTGGCTTAGAGGCTCCCTGTGA
 GGGAGCAGCCCTCCCCAGA**TAA**CCTCTGGAGCAGATTGAAAGCCAGGATGGCGCCTCCAG
 ACCGAGGACAGCTGCCCATGCCCGCAGCTCCTGGCACTACCTGAGCCGGAGACCCAG
 GACTGGCGGCCCATGCCCGCAGTAGGTTCTAGGGGGCGTGCTGCCAGTGGACTGGC
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCTGCTCTGCTGCCAGCAGGGAG
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGCCAGGAGGAAGGGCTC
 TGTGCACTTGCAAGGCCACGTCAAGGAGAGCCAGCGGTGCCCTGTCGGGAGGGTTCCAAGGTGC
 TCCGTGAAGAGCATGGCAAGTTGTCTGACACTTGGTGGATTCTGGTCCCTGTGGACCT
 TGTGCATGCATGGCCTCTTGAGCCTGGTTCTCAGCAGTGAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGG
 GGTGTTGCTGAGGGCTTGTGCCAGGCCAGCCAGAGAGCAGGTGCAGGTGTCACTGGGA
 GAGTTCAAGGCTCTGCACGGCATGGAGTGGGAACCCCACCAAGCTGCTGCTACAGGACCTGGGA
 TTGCCTGGACTCCCACCTTCTATCAATTCTCATGGTAGTCAAACACTGCAGACTCTCAAAC
 TTGCTCATT

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHGHFLLTNLLDKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSCLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVALADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVRREQPLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTCGCGAGCGCTGGC**ATG**TGGTCTGGGCGCGCTGGCGGCTGCTGGCGGTGCTGGCTGGCGCTGAC
GCGCTCGGACAGGAGACCCAGAAAGGGCTCGCGCTGGGGCGACACGTTCTCGGCCTGAC
CAGCGTGGCGCGCCCTGGGCCCGAGCGCCGGCTGCTGGGCTGCTGAGGGCTGAC
GCGGGAGGAGGCGCGCTGGGACCTGACTAGATTCTACGACAAGGTACTTCTTGAT
GAGGATTCAACAAACCCCTGTGGCTAACCTCTGCTGATTACTCTCATCAAACGCCTGCA
GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTGAGGGACCTGAGGGAGCAGCAAGG
GCCCTGATGCGGCTGCAGGACGTGATGCTCAATGTGAAAGGCCTGGCCCAGGGTGTCTT
TCAGAGAGTCAGTGGCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTCTCTCA
CAGGGATGACTGCTCCAAGTTGGCAAGGTGGCTATGACATGGGGATTATTACCATGCC
ATTCCATGGCTGGAGGAGGCTGTCAGTCTTCCAGGATCTACGGAGAGTGGAAAGACAGA
GGATGAGGCAAGTCTAGAAGATGCCCTGGATCACTTGGCCTTGCTTATTCGGGAGGAA
ATGTTCTGTGCCCCCTCAGCCTCTCGGGAGTTCTCTACAGCCCAGATAATAAGAGG
ATGGCCAGGAATGCTTGAATATGAAAGGCTTGGCAGAGAGCCCCAACCACGTGGTAGC
TGAGGCCTGTCATCCAGAGGCCAATATACCCACCTGCAGACCAGAACCTACGAGGGGC
TATGTCAGACCTGGGTCCCAGCCCCTCTACAGATCCCTAGCCTCTACTGTTCTAT
GAGACCAATTCCAACGCTTACCTGCTCCAGCCATCCGAAGGAGGTACCCACCTGG
GCCCTACATTGCTCTTACCATGACTCGTCAGTGACTCAGAGGCTCAGAAAATTAGAGAAC
TTGCAGAACCATGGCTACAGAGGTCACTGGGATCAGGGGAGAAGCAGTTACAAGTGGAG
TACCGCATCAGAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTACCCCTAA
CCACCGCATTGCTGCCCTCACAGGCCCTGATGTCGGCCTCCCTATCCAGAGTATCTGCAGG
TGGTGAACTATGGCATCGGAGGACACTATGAGCCTCACTTGACCATGCTACGTACCAAGC
AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATCTGAGCTC
GGTGGAAAGCTGGAGGAGGCCACAGCCTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
ATGCAGCACTGTTGGAACCTGCACAGGAGTGGTAAGGGGACAGTGACACACTTCAT
GCTGGCTGTCCTGTCCTGGTGGAGATAAGTGGTGGCAACAAGTGGATACATGAGTATGG
ACAGGAATTCCGCAGACCTGCAGCTCCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAC
TGGTGGAGTCCTGTGGCTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGTAGGGAGAGGAGAA
AGCAGAGCAGCCTCTGGAAAGAAGGCCTGTCAGCTTGTGCTGCTCGCAAATCAGAGGC
AAGGGAGAGGTGTTACCAAGGGGACACTGAGAACATGTACATTGATCTGCCCAAGGCCACGGAA
GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAAGTTCTGG
AGTCAGATACTCTGTTGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGGTC
TTTGGCACTTGAACCTTGACCAAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
GGGCTAGCCTGACTCCCAGAACTTAAAGACTTCTCCCCACTGCCTCTGCTGCAGCCAAAG
CAGGGAGTGTCCCCCTCCAGAACATCCCAGATGAGTGGTACATTATAAGGATTTT
TTAAGTTGAAACAAACTTCTTTCTTTGTATGATGGTTTTAACACAGTCATTAAAA
ATGTTATAAATCAAAA

FIGURE 68

MGP GARLA ALLA VLA LAL GTGD PER AARG DTFS ALTS VARA LAP ER LLG LL RRY LR GEE AR L
RDL TRFY DKV LSL HED STTP VAN PLLA FT LIK RL QSD WRN VHS LEASE NI RALK DGY EK VE
QDL PAFED LE GAAR ALM RL QDV YM LN VKG LARG V FQR VTGS AITD LY SP KRL FSL TGDDC FQ
VG KVAY DM GD YY HA IPW LEE AVS LFR GS YGEW KTE DEAS LED AL DHLA FAY FRAG NVSC ALS
LS REFL LYS PDN KRM ARNV LKYER LLA E SPN HVVA E AVI QR PN I PHL QTR DT YEG LC QT LGS
QPT LY QIP SLY CSY ET NS NAY LLQ PIR KEV I HLE PY I ALY HDF VSD SEA QK I REL AEP WL Q
RSV VAS GEK QLQ VEY RISK SAW LKD TVDP KLVT LN HRIA ALT GLD VR PP YAEYL QVV NYGIG
GH YEP HFD HAT SPSS PLY RMK SG NRV ATF MIY LSS VE AGG ATAF IYAN LS VP VVR NA AL FW
NL HRS GEG DSD T L HAG CP VL VG DKW VANK WI HEY GQE FRR PCSS PED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGTTAACGTTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGCC
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCGTAACCCGCGGGGAG
 CGCCCAGG**ATG**CCGCGCGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGCCCTGGTCCT
 GTCTGTGGCATCTATGCAGAGGTTGAGCGGCAGAAATAAAACCTTGAAAGTGCCTTCC
 TGGCTCCAGCCATCATCCTCATCCTCTGGCGTCGTATGTTCATGGTCTCCTTATTGGT
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTGATGTACATCCTGGAT
 CTGCCATCATGGAGCTCATTGGTGGCGTGGCTTGACCTCCGGAACCGAGACCATTG
 ACTCCTGAACGACAACATTGAAAGAGGAATTGAGAACTACTATGATGATCTGGACTTC
 AACATCATGGACTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGAGGACTACCGAGATTG
 GAGCAAGAACATCAGTACGACTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC
 CCTGCTGCATCAGGAACACGACAGAACAGTTGTCAACACCATGTGTGGCTACAAACTATGAC
 AAGGAGCGTTCAGTGTGCAGGATGTACATCTACGTGCAGGCTGCACCAACGCCGTGATCAT
 CTGGTTCATGGACAACACTACACCATCATGGCGTGCATCCTCTGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGTGGAGGACATCATGGAGCAC
 TCTGTCACTGATGGCCTCTGGGCCCGGTGCCAAGGCCAGCGTGGAGGCGGCAGGCACGG
 ATGCTGCTTGTGCTACCCAAAT**TAG**GGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGCTGGACAGGGCTGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCCTGTGTAGGTCCCACGGCTCTGCCTC
 CCCAGGGAGCAGAGCCTGGCCTCCCTAACAGGGCTTCCCGAGGCAGCTCTGGAATCTGT
 GCCCACCTGGGCCTGGGAACAAGGCCCTCTTCTCCAGGCCTGGCTACAGGGAGGGA
 GAGCCTGAGGCTCTGCTCAGGCCATTTCATCTGGCAGTGCCTGGCGGTGGTATTCAA
 GGCAGTTTGTAGCACCTGTAATTGGGAGAGGGAGTGTGCCCTGGGCAGGAGGGAGG
 GCATCTGGGAAGGGCAGGAGGGAAAGAGCTGTCATGCCACGCCATGCCAGGTTGGC
 CTCTCTCAGCCTCCAGGTGCCTTGAGCCCTTGTCAAGGGCGCTGCTCCTTGAGCCTA
 GTTTTTTACGTGATTTGTAACATTGATTTGTACAGATAACAGGAGTTCTGAC
 TAATCAAAGCTGGTATTCCCGCATGTCTATTCTGCCCTCCCCAACAGTTGTTAA
 TCAAACAATAAAACATGTTGTTTTAAAAAAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYWLKFSLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMEIGGVVALTFRNQTIDFL
NDNIRRGNIENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIVVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGGCCGGCCCGTGGACCTCACCCCTCTGTGGTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCCCTGCAGTCTCATCCTCGGCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCCGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCCTGGCCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAATGCTGTATAAGCTCCTCCTGGTAACGCCCTAGCTAAC
 AGGTATGAACCTCCTAGTGCCATCCCTGCCAATCTAGTAAAAACCAGCTGTGTCCCCTG
 ATCGAGGCTCCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTAAGGTGCCATTTC
 CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGTACACCATT
 AGCTCTACCTGGGGCCAAGTTGGACTCACAGGGAAAGGTACCAAGTGGTTCAATAAC
 TCTGCAGCTCCCTGACAATGCCAACCCCTGGACAACATCCGTTAGCCTCATCGTGAGTCA
 GGACGTGGTGAAAGCTGCAGTGGCTGCTGTCTCCAGAAGAATTGATGGTCTGTTGG
 ACTCTGTGCTCCTGAGAGTGCCCATGGCTGAAGTCAAGCATGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGATCTACCCAGATCGTAAGATCCTAACTCAGGACACTCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCAACTGATCGTGTGCTGAAAGTGTTCCTCCA
 GTGAAGGCCCTCCGCCCTTGTTCACCCCTGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTACCAACTTATACTCAACTTGAAATAACATCAGCTCTGATCGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAGATCTGGGGTCCCAGTGTATTGGT
 AAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCC
 AGCCTCCTGTGGAAACCCAGCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGTCCCAGCTGGAGTATGGGTGTGAGCTATAGACCATCCCTCTGCAAT
 CAATAAACACTTGCCGTGAAAAA

FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM
REKPAGGIPLGLSVNTVLKHIWLVKVTANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQILLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFNNSAASLTMPTLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNINNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSRGVPVSLVKALGFEAAESSLTKDALVLTPASLWKPSSPVSQ
```

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**ATG**GCAGCGCGTGGCGTTGGTGTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTGCGACGTTCCCTCAGCCTCTGCCAAAGAAAGAAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTCCCGTGCCTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAAGTGCATAGACAGTGTGCGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AAACTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTGCCATGGTGGATTTG
 ATGAAGGCTCTGATGTATTCAGATGCTAACATGAATTCACTGCTTCAACTTT
 CCTGCAAAAGGGAAACCCAAACGGGGTGTACATATGAGTTACAGGTGCAGGGTTTCAGC
 TGAGCAGATTGCCCGGTGGATGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCTATGTTGGGATTGCTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTCGAAGAAGTAATATGGAATTCTCTTTAATAAAACTGGATGGCTTGCAGCTTGTG
 TTTTGTGCTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACACCATAAGCCC
 ATAAGAATCCCCCACAGGGACATGTGAATTATATCCATGGAAGCAGTCAAGGCCAGTTGTA
 GCTGAAACACACATTGTTCTCTGTTAATGGTGGAGTACCTTAGGAATGGTGTGGCTGGTATTG
 TGAAGCTGCTACCTCTGACATGGATATTGAAAGCGAAAGATAATGTGTGGCTGGTATTG
 GACTTGTGTATTATTCTCAGTTGGATGCTCTATTAGATCTAAATATCATGGCTAC
 CCATACAGCTTCTGATGAGT**TAA**AAAGGTCCCAGAGATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTTGAAAAGAAGAATGCAACTTGTATATTGTATTAC
 CTCTTTTTCAAGTGATTAAATAGTTAATCTAACAAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTGAAAATAATTATCCTCTAACCTCTCTT
 CCCAGTGAACTTATGGAACATTAAATTAGTACAATTAAAGTATATTAAAAATTGTAAAAA
 CTACTACTTGTGTTAGTTAGAACAAAGCTCAAAACTACTTAGTTAACTGGTCATCTGAT
 TTTATATTGCCTTATCCAAAGATGGGAAAGTAAGTCCTGACCAGGTGTTCCCACATATGCC
 TGTACAGATAACTACATTAGGAATTCTAGCTTCTCATCTTGTGGATGTGTAT
 ACTTTACGCATCTTCTTGTAGTAGAGAAATTATGTGTGTATGTGGTCTTCTGAAAATG
 GAACACCATTCTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTCTCCTCCT
 GCATATTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAGTA
 TCTCTAAATACAGGATTATAATTCTGCTTGAGTATGGTGTAACTACCTGTATTAGAAA
 GATTCAGATTCCATCTCCTTAGTTCTTAAGGTGACCCATCTGTGATAAAAATA
 TAGCTTAGTGCTAAATCAGTGTAACTATACATGGCTAAAATGTTCTACAAATTAGAGT
 TTGTCACTTATTCCATTGTACCTAAGAGAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGACTTACGCCGTAACTCAGCACCTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTAGGAGTTCGAGACCATCCTGCCAACATGGTGAACACCCGTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACTCAGGAGATGGAGGTTCACTGAGCCGAGATCACGCCACTGCACTCC
 AGCCTGGCAACAGAGCAGACTCCATCTCAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQMEWTNKRPVIRMNGDKFR
RLVKAPPNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALAFCVLAMTSQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAATGCAAGCTTGGGAGTTGTCGCTGCCCTGCCGTCTGCTAGGGAGA
 GAACGCCAGAGGGAGGCAGCGCTGGCCCGGCAGGCTCTCAGAACCGTACCGCG**ATG**CTA
 CTGCTGTGGGTGTCGGTGGCGCAGCCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA
 GCAGAGGCAGGAGAGCAGCCAAGCGCCAATGTGGTGCTGGCGTGAAGCGACTCCTCGATG
 GAAGGTTAACATTTCATCCAGGAAGTCAGGTAGTGAACACTTCCTTTATCAACTTATGAAG
 ACACGTGGACTTCCTTCTGAATGCCACACAAACTCTCAATTGTTGCCATCACGC
 AGCAATGTGGAGTGGCCTTCACTCACTTAACAGAACATTTAAGGGTAG
 ATCCAAATTATAACACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATT
 GGGAAACTGGACTATACTCAGGACATCACTCCATTAGTAATCGTGTGGAGCGTGACAAG
 AGATGTTGCTTCTTACTCAGACAAGAAGGCAGGCCATGGTTAATCTTATCCGAACAGGA
 CTAAGTCAGAGTGATGGAAAGGGATTGGCAGAACATACAGAACAGACTAAACTGGTTAAGA
 AAGGAAGCAATTAAATTACACTGAACCATTGTTATTACTGGGATTAAATTACACAC
 TTACCCCTCACCATCTGGAGAAAATTGGATCTCAACATTACACATCTCTTATT
 GGCTGAAAAAGTGTCTCATGATGCCATCAAAATCCAAAGTGGCACCTTGTCAAGAAATG
 CACCTGTAGATTATTACTCTTACAAAAAAACTGCACTGGAAGAGATTACAAAAAAAGA
 AATTAAGAATATTAGAGCATTATTATGCTATGTGTGCTGAGACAGATGCCATGCTGGT
 AAATTATTTGGCCCTTCATCAATTAGATCTTCTCAGAAAATATTGTCAATACCTCA
 GACCATGGAGAGCTGCCATGGAACATCGACAGTTTATAAAATGAGCATGTACGAGGCTAG
 TGCACATGTCGCTTTGATGATGGGACCAGGAATTAAAGCAGGCCTACAAGTATCAAATG
 TGGTTCTTGTGGATATTACCTACCATGCTGATATTGCTGGAATTCTCTGCCCTCAG
 AACCTGAGTGGACTCTTGTGGCTTACATCAGAAACATTAAAGAACATCAAAGT
 CAAAAACCTGCATCCACCCCTGGATTCTGAGTGAATTCCATGGATGTAATGTGAATGCC
 CCTACATGCTCGAACTAACCACTGGAAATATATAGCCTATTGGATGGTGCATCAATATTG
 CCTCAACTCTTGATCTTCTCGGATCCAGATGAATTAAACAAATGTTGCTGTAAATTCC
 AGAAATTACTTATTCTTGTGGATCAGAACGCTTCATTCAACTACCCCTAAAGTTCTG
 CTTCTGTCCACCAGTATAATAAGAGCAGTTATCAAGTGGAAACAAAGTATAGGACAGAAT
 TATTCAAACGTTATAGCAAATCTAGGTGGCACCAAGACTGGCAGAAGGAACCAAGGAAGTA
 TGAAAATGCAATTGATCAGTGGCTAAAACCCATATGAATCCAAGAGCAGTT**TGA**ACAAAAA
 GTTAAAAAATAGTGTCTAGAGATACATATAAATATTACAAGATCATAATTATGTATT
 AAATGAAACAGTTTAATAATTACCAAGTGTGGCCGGCACAGTGGCTCACACCTGTAATC
 CCAGGACTTGGGAGGCTGAGGAAGCAGATCACAAGGTCAAGAGATTGAGACCACCTGGC
 CAACATGGTGAACACCTGTCTACTAAAAATACAAAATTAGCTGGCGCGGTGGTGCACA
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGGAGGATCGCTTGAACCCGGGAGGCAGCAG
 TTGCAGTGGCTGAGATTGCCACTGTACTCCAGCCTGGCAACAGAGTGGACTGTGCG
 AAAAATAAAAATAATAATTACCAATTTCATTATTGTAAAGAATGTAGTG
 TATTAAAGATAAAATGCCAATGATTATAAAATCACATATTCAAAATGGTTATTATT
 GCCCTTGTACAATTCTAACAAATTAGTGGAGTATCAAAGGATTGAAGCAAATACTGTA
 ACAGTTATGTTCTTAAATAATAGAGAATATAAAATTGTAAATATGTATCATAAAAT
 AGTTGTATGTGAGCATTGATGGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAA

FIGURE 76

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLLRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQQLDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSVLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELTNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIWKQSIG
QNSNVIANLRWHQDWQKEPRKYENAIQWLKTHMN PRAV

```

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTGGCCTCCAACTTGTGGCTACATCCTAGGCCTCTGGGGCTTTGGGCACACT
 GGTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG
 CAGTTGGCTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATACCCAG
 TGTGACATCTATAGCACCCCTCTGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTTGGCATGAGATGCA
 CAGTCTCTGCCAGGAATCCCGAGCAAAGACAGACTGGCGTAGCAGGTGGAGTCCTTTTC
 ATCCTTGGAGGCCTCTGGGATTCAATTCTGTTGCCCTGGAAATCTCATGGGATCCTACGGGA
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTGAGATTGGAGAGGGCTTTACTTGG
 GCATTATTCTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACACTACGATGCCAACCTCTGCCACAAGGGAGCTC
 TCCAAGGCCTGGTCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
 ATGTG**TGA**AGAACCAAGGGCCAGAGCTGGGGGTGGCTGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTCAGAAGGTGCTGCTGAGG
 ATAGACTGACTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTGCCATGCCAGCCTCTGTTCTCACCTTGCTGCTC
 CCCTGCCCTAACGCCCCAACCTCAACTTGAAACCCCATTCCCTAACGCCAGGACTCAGAGG
 ATCCCTTGCCCTCTGGTTACCTGGACTCCATCCCCAACCCACTAACATCACATCCACTG
 ACTGACCCCTCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTTAGCTCATTGCTGG
 GGATGGGAAGGGAGAACAGTGGCTTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCACTCTGTTATGACTCCACAGTGTCC
 AGACTAATTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGACATTAAAAAAATA

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLGLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGISSLFSLIAGIILCFSCS
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
```

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCAC TGCT GCT GTCCC ATCAG CTGCT CTAAG CTCC **ATG** GTGCC CAGA ATCT CGCT CCTGC
TTAT GTGT CAGT CTGT CTCC CTCT TTGT GTCCA AGGG AAGT CATCG CTCC GCT GGCT CAG
AACCAT GGCT GTGCC AGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTGGAGCAG
TGCT GTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTGAGCTCTGCTGTCTTGATTCCCTTGGCCTCACAAACGATTGTTG
TGAAGCTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTCCCT**TGA** GAAGACATAGAAAGAAAATCAACTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTATATGTGTACCA GTAGAGAAGCCTGAGGAATTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAAAGTGGTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRIFAPAYVSVC~~LLL~~C~~P~~REVIAPAGSEPWLCPAPRCGDKIYNPLEQCCYND~~A~~IVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFVVKLKVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

FIGURE 81

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT
GCTATGATGATGCCCGTCGTGCCCTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTGAGCAGTGCTGCCCTGGACCTTCATGGTAAGCTGATAAACAGAACTGCGA
CTCAGCCCAGCTCGGATGACAGGCTTGTGCGAGTGTCACT**TAA**TGGAACATCAGGGAA
CGATGACTCCTGGATTCTCCTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTGGGGCCAGAGAAACACACACTCAACTGCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCCTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGCCAGGGACTCTGAACCCCTCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCCCAAGGCTGGCTGGGAACCCCTCACCC
TCTGTGAGATTTCCATCATCTCAAGTTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM CQPHKRCGD KFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVC FEQCCPWT FMVK L INQN CDSARTS DDL CRSVS

Signal peptide:

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGTGGGCCGCCGCAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTCCCCGCGCCGGCGTCCCGCCCCTCCCCGGCACCAAGATTCCTCT
 GCGCGTCCGACGGCGAC**ATG**GGCGTCCCCACGCCCTGGAGGCCGGCAGCTGGCGCTGGGA
 TCCCTGCTCTCGCTCTTCCCTGGCTCGTCCCTAGGTCCGGTGGCAGCCTCAAGGTCGC
 CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGAGAACGTACCCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTACAAGACGTGGTACCGCAGCTCGAGG
 GGCGAGGTGCAGACCTGCTCAGAGGCCGGCCATCCGAAACCTCACGTTCCAGGACCTCA
 CCTGCACCAGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTAGGCCACGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGAACCTGACCCCTGCTG
 GATAGCGGCCTACTGCTGCCTGGTGGAGATCAGGCACCACACTGGAGCACAGGGT
 CCATGGTGCCTGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACACTGTGTGGTGT
 ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCCGTGCCAGGAGCTGGTGCAGACAGCAACATTCAAGGGATTGAAAACC
 CCGGCTTGAGCCTCACCACCTGCCAGGGATAACCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTCTGAGTCTGGCGGCATCTGCTTCGGAGCCAGCAC
 CCCCTGTCTCCTCCAGGCCCGAGACGTCTTCCATCCCTGGACCCCTGACT
 CTCCAAACTTGAGGTCACT**TAG**CCCAGCTGGGGACAGTGGCTGTTGGCTGGTCTGG
 GGCAGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTGGCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGCTCAGATACTGTGACATCCCAGAACGCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTGGGTGCTGAG
 ATTCTCCCCTAGAGACCTGAAATTCACAGCTACAGATGCCAAATGACTTACATCTAAGAA
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTCGTTCTGAGACATGAGCCTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCCTCCAGGCACCAGACACAGGGCACGGT
 GAGAGACTCTCCCCGTGGCGCCTGGCTCCCCGTTGCCAGGCTGCTCTGTG
 AGACTTCCTTTGTACCACAGTGGCTCTGGGCCAGGCCTGCCACTGCCATGCC
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTCTGAAGATCTGCAACAGGTTAAGTCAAT
 CTGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTGGTGGTCCGAAACGGGAAGTAC
 ATATTGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCAACCACTGGAGATGGTGTGAGGGAGGTGGTGGGCCCTCTGGGAAGGTGA
 GTGGAGAGGGCACCTGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCACACAATGTCTGTCCACCCCTGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAAACTACATGGGAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSEERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSQ
DSENITAAALATGACIVGILCLPLLLLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPPGDVFFPSLDPPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTCGTCTCCATCTCTCCCTCCT
 TTCCCCGCGTTCTCTTCCACCTTCTCTTCTCCCACCTTAGACCTCCCTGCCCTCC
 TTTCTGCCAACGCGTCTGCCCTGGCCCTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCCTTCGTCTCCCTCCGA
 CTCCGCTCCCGGACCAGCGGCCTGACCCCTGGGAAAGG**ATG**GTTCCCGAGGTGAGGGTCCTC
 TCCTCCTTGCTGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCGCC
 AGACATGTTCTGCCTTCCATGGAAAGAGATACTCCCCCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGGCCCATGTGAGT
 TGTACCGCCTCCACTGTCCGCCTGTCCACTGCCCTGACGGAGCCACAGCAATG
 CTGTCCAAGTGTGTGGAACCTCACACTCCCTGGACTCCGGGCCCCACCAAAGTCCTGCC
 AGCACAAACGGGACCATGTACCAACACGGAGAGATCTCAGTGCCATGAGCTGTTCCCCTCC
 CGCCTGCCAACCAGTGTGTCCCTGCAGCTGCACAGAGGGCCAGATCTACTGCCCTCAC
 AACCTGCCCGAACCAAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAACGCT
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGGCCGGCACCCAGC
 CCCACTGGCCTCAGGCCCTCTGAGCTTCATCCCTGCCACTCAGACCCAAGGGAGCAG
 GCAGCACAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTACTCCCACGGGAGGTGTGGCACCCGGCTTCCGTGCCTCGGCCCTGCCCTG
 CATCCTATGCACCTGTGAGGATGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCAGAGGACAAA
 GCAGACCTGGCCACAGTGAGATCAGTTCTACCAGGTGCTCCAAAGGCACCGGGCGGGTCT
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTGCCTGGAACACGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAACTTCCACTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCAC
 GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCCTGGAGCTGAAGGTACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGAC**TAA**CAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAGAAGTTGCATTACCCCTAAAAAAAAAAAAAA

FIGURE 86

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPGTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV
KDETEAQRGEVPGPRPHSQNLPLSDQESQEARNPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGAACAGCTTGC GGCTGC GGGGAGCTCCC
GTGGCGCTCCGCTGGCTGTGCAGGCGGCC**ATG**ATTCTTGC GGAAAATGCTGATCTCAGT
CGCAATGCTGGCGCAGGGCTGGCGTGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG
AGCGGCAGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAGGAGCAGGGAGGAG
GCGGCCAGGACCCAGCAGCTATTGCTGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAACTGGATGGTTGGCGCGAAGGC GGCGCCAGCGGGAGGTACCG**T**
GA GACCGGACTTGCCTCCGTGGCGCCGGACCTTGGCTTGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTTCGTGGGCCAGCGGAGAGTCCGGACCGAGATAACCATGCCAGGACTCTCCGGGG
TCCTGTGAGCTGCCGTGGGTGAGCACGTTCCCCCAAACCTGGACTGACTGCTTAAGGT
CCGCAAGGC GGCCAGGCCAGACGCGAGTCGGATGTGGTAAGTGAACGAAAGAACCAATAAAA
TCATGTTCTCCAAAAA AAAAAAAAAAAAAA AAAAAAAAAAAAAA AAAAAAAAAAAAAA
AAAAAAAAAA

FIGURE 88

MDSLRKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

FIGURE 89

CAGGAGAGAAGGCACCGCCCCCACCCGCCTCAAAGCTAACCTCGGGCTTGAGGGAAAGA
GGCTGACTGTACGTTCTTCTACTCTGGCACCCTCTCCAGGCTGCC**ATG**GGGCCAGCACC
CCTCTCCTCATCTTGTCCCTTGTCAATGGCAGGGACCCCTCCAAGGACAGCAGCACCACCT
TGTGGAGTACATGGAACGCCGACTAGCTGCTTAGAGGAACGGCTGCCAGTGCAGGACC
AGAGTAGTCGGCATGCTGCTGAGCTGCAGGGACTTCAAGAACAGATGCTGCCACTGCTGGAG
GTGGCAGAGAAGGAGCAGGGAGGCAGTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGG
TCGTCTGGAGCAGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTGAGAGT
TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAAGAAGGAATGAGAAGTAC
GATATGGTACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG
ATTGGTGGCCCAGCTGGTCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACG
TGTAGATGGACACAGAACATGACACAGCCTTGTCTTCCAAAGGCTGCGTGACTTCACCC
GCCATGGCTGCCCGAAAGCTTCCCGAGTCCGGTGCCCTCCCTGGTAGGCACAGGGCA
GCTGGTATATGGTGGCTTCTTATTTGCTCGGAGGCCTCTGGAAAGACCTGGTGGAGGTG
GTGAGATGGAGAACACTTGACGTAATCAAATTCCACCTGGCAAACCGAACAGTGGTGGAC
AGCTCAGTATTCCAGCAGAGGGCTGATCCCCCTACGGCTTGACAGCAGACACCTACAT
CGACCTGGTAGCTGATGAGGAAGGTCTTGGCTGTCTATGCCACCCGGGAGGATGACAGGC
ACTTGTGTCTGGCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCA
TGTCCAGAGAGAACATGCTGAGGCTGCCTTGTCACTGTGGACCCCTATGTCGTATAAA
CACCCGTCCTGCCAGTCGGGCCCGCATCCAGTGCTCCTTGATGCCAGCGGCACCCGTACCC
CTGAACGGGCAGCACTCCCTATTTCCCGCAGATATGGTGCCTATGCCAGCCTCCGCTAT
AACCCCCGAGAACGCCAGCTATGCCCTGGATGATGGCTACCAGATTGTCTATAAGCTGGA
GATGAGGAAGAAAGAGGAGGAGGTT**TGA**GGAGCTAGCCTGTTTGATCTTCTCACTC
CCATACATTATATTATATCCCCACTAAATTCTTGTCCCTATTCTCAAATGTGGCCAG
TTGTGGCTCAAATCCTCTATTTAGCCAATGGCAATCAAATTCTTCAGCTCCTTGT
TCATACGGAACTCCAGATCCTGAGTAATCCTTAGAGGCCGAAGAGTCACAAACCCCTCAATG
TTCCCTCCTGCTCTGCCCATGTCAACAAATTCAAGGCTAAGGATGCCAGACCCAGG
GCTCTAACCTGTATGCCAGGGCAGGCCAGGGAGCAGGCAGCAGTGTCTCCCTCAGAGTG
ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCTGTCCCTCTTCCCTCACTCCTCCCT
TCAGTGTCCCTGAGGAACAGGACTTCTCACATTGTTGTATTGCAACATTGCAATTAAA
AGGAAAATCCACAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSGPLQGQQHHLVEYMERLAALERLAQCQDQSSRHAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDTVLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIVVLDGTQNDTAFVFPR
RDFTLAMAARKASRVRVFPFWVGTLGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ
QWDTPCPRENAAAFVICGTLVVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTCCATGCCGTGAGGCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTGGTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTT
 GGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAGGACGCAGCATTCTCCTGTTCTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTGCACAGTATCAAGGCAGG
 TCCACCTCTACAGGGACGGGAGGACCAGCATTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAAACTGGTGAAGGATTCTATTGCGGAGGGCGCATCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGCCCTATGGGTGCAGGATTAGTCCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGCCTCAGTTCTCATTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCAGTCCTCAGGCTGGTCCCCGGCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGCC
 TGTTGATGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTCGA
 GCCTATATCGTGGCACCTGGTACCAAAGTACTGGGAAACTCTGCTGTGGCTATTTTG
 GCATTGTTGGACTGAAGATTCTTCTCCAAATTCCAGTGGAAAATCCAGGCAGGAACTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTACCCGAAGCTCTGCGTTCTGATCTGAAAATGTAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAGGTG
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTGTCTCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTGTATTTCACATTAAATCCCCGT
 TTTATCAGCGTCTCCCCAGGACCCCACCTACAAAAATAGGGTCTCCTGGACTATGAGTG
 TGGGACCATCTCCTCTTCAACATAATGACCAGTCCCTATTATACCCCTGACATGCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAATGGAACCTCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCTTGGCAAAGGGCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTCCTCCCCAGGG
 GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTAGGGATATTAAGGTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGGCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTATGGCTGCCCTGAGCTGGAGGGAAAGAAGGCTGACATTACATT
 AGTTGCTCTCACTCCATCTGCTAAGTGATCTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTGTCATTATATTACACTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGGSGQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQK
AIWELQVSALGSVPPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPQGQDLSTDRTNRDMH
GLFDVEISLTQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTL
PDHGywvLRLNgeHLYFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYEQNGTPIVICPVTQESEKEASQRASAIPESTNSSESSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCGGTGGCGGTGGCGGCGGGTTGCGGAGGCTTCCTGGTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGC
CATGAGGAGCCTGCCGAGCCTGGCGGCCTGCCCTGTGTGCTGCGCCGCCGCCGCC
 CCGTCGCCTCAGCCGCCTCGGCGGGGAAATGTCACCGGTGGCGGGGGCCGCCGGGGCAGGTG
 GACGCCTGCCGGGGCCCGGGTTGCGGGGGCGAGCCCAGCCACCCCTCCCTAGGGCGACGGC
 TCCCACGGCCCAGGGCCCCGAGGACCGGGCCCCCGCGGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGGCCAGTCCCCGGAGACCACCCCTTTGGCGACTGCTGGACCCCTTCC
 ACCACCTTCAGGCGCCGCTGGCCCTCGCCGACCACCCCTCCGGCGGCGAACGCACTTC
 GACCACCTCTCAGGCGCGACCAGACCCCGCGACCACCCCTTCGACGACCACGGCCCG
 CGCCGACCACCCCTGTAGCGACCAACCGTACCGCGCCACGACTCCCCGGACCCGACCCCC
 GATCTCCCCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC
 TTGCGCTCCTCCAGAGTATGTAACTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGGCAGTGTGAGTGTGGCCAGGTATCAGGGCTTCACTGTGAAACC
 TGCAAAGAGGGCTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAACTGAAGTTATT
 TTATTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGTTAAACAAAG
 GAGGATGAGGGTCAAGATTACAAAATATTTATATACTTTATTCTCTACTTTATATGT
 TATATTAAATGTCAGGATTAAAAACATCTAATTACTGATTTAGTTCTTCAAAAGCACTAG
 AGTCGCCAATTTCTGGATAATTCTGTAAATTCTAGGGAAAAATTATTGAAGAAT
 AAATCTGCTTCTGGAGGGCTTCAGGCATGAAACCTGCTAGGAGGTTAGAAATGTTCTT
 ATGTTATTAAATATACCATGGAGTTGAGGAAATTGTTGTTGGTTATTCTCTCTA
 ATCAAATTCTACATTGTTCTGGACATCTAAAGCTTAACCTGGGGTACCTAATT
 TTTAACTAGTGGTAAGTAGACTGGTTACTCTATTACAGTACATTGAGACCAAAAG
 TAGATTAAGCAGGAATTATCTTAAACTATTATGTTATTGGAGGTAATTAAATCTAGTGG
 ATAATGTACTGTTATCTAACGATTTGCCCTGTACTGCACTGAAAGTAATTATTCTTGACCT
 TATGTGAGGCACTGGCTTTGTGGACCCCAAGTCAAAAAACTGAAGAGACAGTATTAAAT
 AATGAAAAAAATAATGACAGGTTAACTCAGTGTAACTGGTATAACCCAAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTGGCAAGTAATTCTTCACTGAGCTTGTGTTCTCTCAAG
 GTTGTGTGAAGATTAATGAGTTGATATATAAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGGTTGTTAATTCAAAGGAATTATGGACTGAAATGAGAGAACATGTTAAGA
 ACTTTAGCTCCTGACAAAGAAGTGTAACTTTAGCACTAAATATTAAATGCTTTA
 TAAATGATATTATACTGTTATGGAATTATTGTATCATATTGTAGTTATTAAAAATGTAGAAG
 AGGCTGGCGCGGTGGCTACGCCTGTAATCCTAGCAGCTTGGGAGGCCAAGGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTACTAAA
 AATACAAACAAATTAGCTGGCGTGGCACACACCTGTAGTCCCAGCTACTGGGAGGCT
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCACTGAGCTGAGATCGGCCACT
 GCACCTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTAAAAAAAAAAAAAA

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSILPSLGGIALLCCAAAAAVASAASAGNVTGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTPAAERTS
TTSQAPTRPAPTTLSTTGAPTPVATTVPAPTPRTPTPDLPSSNSSVLPTPPATEAPS
SPPPEYVCNCNVGSINVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTCTGGCTTG
TCTCGGTGCCAGGGCCCAGGCCGTGGTTGGGAAGACTGGACCCCTGAGCAGCTCTGGG
CCCTGGTACGTGCTTCGGTGGCCTCCGGAAAAGGGCTTGCCATGGAGAAGGACATGAA
AACGTCGTGGGGTGGTGACCCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTGAGAATCCCTCAATAGCGTGCTGGAGCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTCACTCAGCTGGAGTCGGGACGAGCCCTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGGCCAGGAGGCCATGGGCTTCAACAGTGGAGCAGGAGC
CTGGGCTTCGTACAG**TAG**CAGGCCAGCTGCAGAAGGACCTCACCTGTGCTACAAGAT
CCTTCTGTGAGTGCTCGTCCCCAGTAGGGATGGCGCCACAGGGCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

FIGURE 96

MGGLLLAFLALVSVPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRITLSSQHGLGGCDQSVMMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGGGCCCTGGCACCTCTAACCCCAGAC**ATG**CTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCCTGTGTGCCATGTGCCCTGCTCCTCTCCTACCCCTCGCAT
 GGCTGGATTACCCCTGGCCCAGTAGTCATGGCTACTGGTTCCGGGAAGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTGGCAGTGTGGAGGAGACTCGGGACC
 GATTCCACCTCCTGGGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCCAG
 GCACCCCTGGAGTCCGGCTGCCCTCAGAATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAG
 GGGACACCCCCATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTCACCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGCCAGCGTGACCACGAACAAGACCGTCCATCTAACGTGTCCTAC
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTGTCACTCCCAGAGGGCCAGTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCTGTGCC
 TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCCTGGGTGCACCTGAGGGATGCAGCTGA
 ATTTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGAGCTGGAGGCCACAGCCCTG
 GTCTTCCCTGTCCTCTCGTCATCTCGTTGAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGAGATAAGGGCATAGAGGATGCAAACGCTGTCAGGGGTTCAGCCT
 CTCAGGGGCCCTGACTGAACCTGGCAGAACAGACAGTCCCCCAGACCAGCCTCCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGAGGGAGAGCTCCAGTATGCATCCCTCAGCTTCAGATGGT
 GAAGCCTTGGGACTCGCGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGA**TGA**GAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTGTAGAATTAAACAGCCCTAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTAGAGTCAAAGTATCTAAACCTGAAT
 CCACACTGTGCCCTCCCTTTATTTTTAACTAAAAGACAGACAAATTCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPSCFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTL SIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMTVFQGDG
TVSTVLGNSSLSLPEGQSLRLVCAVDADSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVR
CRKKSARPAAGVGDTGIEDANAVRGASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCAGTGACCTGCCGAGGTGGCAGCACAGAGCTCTGGAG**ATGA**AAGACCCTGTTCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTCACCCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAAGGACTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAAGGTGACAGCCCTGGCGGTGGGAAGTTGGAAGGCCACGTTCACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCAC
ACATCTTTACTGCAAAGACCAGCACCATGGGGCCTGCTCCACATGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCAGGGAGGCCCTGGAAGAATTAAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGGAGGACATTTCACGCCCTGCAGACGGGAAGCTGCCTCCGAACAC**TAGG**
CAGCCCCGGGTCTGCACCTCCAGAGCCCACCCCTACCACAGACACAGAGCCGGACCACCT
GGACCTACCCTCCAGCCATGACCTTCCCTGCTCCCACCCACCTGACTCCAAATAAGTCCT
TTTCCCCCAAAAAAAAAAAAAAAA

FIGURE 100

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

Important features:

Signal peptide:

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCGCTCCTCCCCCTCCAGGCC**TAG**AGGATTCTGCAGTTAA
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTTCGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
GGCGACGCTCATGCCCGAGATGGCTCCTGACAGCAGCCCAGTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGCAGCACAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTCCCCACCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCAGTGCCTGCACACCTGCAGCTGCCTCATTCGGCTGGGCAGCACGTCC
AGCCCCCAGTTACGCCTGCCTCACACCTGCAGCTGCCTCACACCATCATTGAGCACCA
GAAGTGTGAGAACGCCTACCCGGAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGAUTCCGGGGCCCTCTGGTCTGTAACCAGTCTTT
CAAGGCATTATCTCCTGGGCCAGGATCCGTGCGATCACCCGAAAGCCTGGTGTACAC
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAAT**TAG**ACTGGACCCA
CCCACACAGCCCATCACCCCTCCATTCCACTGGTGTGTTGGTCTGTTCACTCTGTTAAT
AAGAAACCTAACGCAAGACCCCTACGAACATTCTGGCCTCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTGTTCTGTTGTATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGGTTCAATAAATATTGCTAAATGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGETRIIKGFECKPHSQWQALFEKTRLLCGATLIAPRWLLTAH
CLKPRYIVHLGQHNLQKEEGCEQRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGSCLISWGSTSSPQLRLPHTLRCANITIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDSGGPLVCNQSLQGIISWGQDPCAIRKPGVYTKVCKYVDWIQETMKNN
```

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTCTGCTGGAGCCG**ATG**CCAAAACCATGCATTCTTATTCA
GATTGTTTTATCTGTGGGCCTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAACGTTGCATCGTCAGAAAAGCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCAAATGGTTGTTCTGGTGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATA
CCCCCTTCATTGTCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATT
AGATTGAACTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGATTGAA
AAAAGATGAGAACGCCACGTGACAAGTCATATCAGGATGCAGTTAGAAGATATTTTAAGA
AGAATGACCATGATGGTATGGCTTCATTCTCCAAGGAATACAATGTATACCAACACGAT
GAACTA**TAG**CATATTGTATTCTACTTTTTTTAGCTATTACTGTACTTATGTATA
AAACAAAGTCACTTCTCCAAGTTGTATTGCTATTCCCCTATGAGAACGATATTTGA
TCTCCCCAATACATTGATTTGGTATAATAATGTGAGGCTGTTGCAAACTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIEFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDFISPKEYNVYQHDEL
```

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAA**ATG**CAGGGACCATTGCTTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTGGAGCT
GTGACTCAGAAAACCAAAACTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGCAGAAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCCAGTTCTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTAGGAGTTGAGACCAGCCTGGCCAACATAGTGAACAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGCGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCAGGAGAATCGCTGAACTCAGGAGGCAGAAGTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTAAAAAGAAAAGA
TAGTTTCTTGTTCATTCGCGACTGCCCTCTCAGTGTTCCTGGATCCCCTCCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSR

Signal peptide:

amino acids 1-18

FIGURE 107

CAAGCAGGT CATCCCCTGGTGACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTCCCCCAGACTTGGAA GTGACCCACCATGG
GGCTCAGCATCTTTGCTCCTGTGTCTGGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGCGTA ACTCACAGCCGTGGCAGGTGGGCTGTTGAGGGCAC
CAGCCTGCGCTGCGGGGTGTCCTATTGACCACAGGTGGGT CCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGGTGCGCCTGGGGAACACAGCCTCAGCCAGCTGACTGGACCGAG
CAGATCCGGCACAGCGGCTCTGTGACCCATCCGGTACCTGGGAGCCTGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCGTCCGCGTAACCAGCAGCGTTCAAC
CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGC
ATCACCAACCACCCACGGAACCCATTCCGGATCTGCTCCAGTGCCCTAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTATCCGGAGAACATCACGAGCAACATGGTGTGTCAG
GCGCGTCCGGGCAGGATGCCTGCCAGGGT GATTCTGGGGCCCCCTGGTGTGGGGGA
GTCCTCAAGGTCTGGTGTCTGGGGCTGTGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAATGAC
CTGTTCTCCACCTCCACCCCCACCCCTTAAC TTGGGTACCCCTCTGCCCTCAGAGCACC
AATATCTCCATCACTCCCTAGCTCCACTCTGTTGGCCTGGAACCTCTTGGAACTT
TAACTCCTGCCAGCCCTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAAATATAAATGAAGGAGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCLVGLSQATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITHNPRNPFPDILLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDGGPLVCGGVLQGLVSWGSVGPGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGAGCCCCGCGCTGCC**ATG**TGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGAAGGCCTGGCTGCTCAAAGCCGGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGGAGTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTCCAGAAAA
 GCTCACAGCCTCAAAGAGAAGTACATGGAGTTGACCTGAACAATGAAGGCAGATTGACC
 TGATGTCTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGTCAGTGACACTATATCCTACCGAGACTTGTGAA
 CATGATGCTGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCC**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTCCCACCCATACCTCCCTCCGATCTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCATTTGTTGGCATTGAGGGTTGTTGTGTT
 TCATCAATGTCTTGTAAAGCACAAATTATCTGCCTAAAGGGCTCTGGTCGGGAATCC
 TGAGCCTTGGTCCCCCTCTCTTCTTCCCTCCCTCCGCTCCGTGCAGAAGGGCTG
 ATATCAAACCAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTTCAAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTTTGGTTCTTGGACAGTGCCTGGTCCAGTGCTCTGGTGTGCACCC
 AGGACACAGCCACTCGGGCCCCGCTGCCAGCTGATCCCCACTCATTCCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGAAAGGAAAGGAGCTTGGCATTGGAGCCCTCAAGAAGG
 TACCAAGGAACCCCTCCAGTCCTGCTCTGCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTACTGGGGCAGCAGAGGGCTCGGAGGCAGAAGTGAGGGCTG
 GGGTTGGGGAAAGGTAGCTCAGTGCTGTTCCACCTTGTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTTGCTGTGACCCCAATCTGCTTGAaaaaaaaaaaaaaaa

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTA
FKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMM
MLGKRSAVLKLVM
MFEGKANESSPKPVGPPP
ERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCCCTCCTCGGGCTCCACCGCTCTGCCCGCAGAGGCAGCCTCCTCCA
 GGAGCGGGGCCCTGCACACC**ATG**GCCCCCGGGTGGCAGGGTGGCGCCGTGCGGCC
 CGCCTGGCGCTGGCTTGGCGCTGGCGAGCGTCTGAGTGGCCTCCAGCGTCGCTGCC
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGCTGGCCTCCGCGCGGTT
 CTCGGGGCATCCCCGCAACGCTGAGCGCTTGACCTGGACAGAAATAATACCAAGGATC
 ACCAAGATGGACTTCGCTGGGCTAAGAACCTCCGAGTCTGATCTGAAGAAGACAACCAGGT
 CAGCGTCATCGAGAGAGGCGCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCTGAACA
 AGAATAAGCTGCAAGCCTCCAGAATTGCTTCCAGAGCACGCCAGCTCACCAGACTA
 GATTGAGTAAAACAGATCCAGGGATCCCAGGAAGGCGTCCGCGGATCACCGATGT
 GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTCCGAGCGC
 TCGCGATTGGAGATCCTTACCCCAACAACAACATCAGTCGCATCTGGTCAACCAGC
 TTCAACCACATGCCGAAGATCCGAECTGCGCCTCCACTCCAACCACCTACTGCGACTG
 CCACCTGGCCTGGCTCTCGGATTGGCTCGACAGCGACGGACAGTTGGCAGTTCACACT
 GCATGGCTCCTGTGCATTGAGGGCTTCAACGTGGCGATGTGAGAAGAAGGAGTACGTG
 TGCCCAGCCCCCCTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTCGCC
 CTGCACTGTGCAGCAATAACATCGTGGACTGTCAGGAAAGGGCTTGATGGAGATTCTGCCA
 ACTGCCGGAGGGCATCGTCAAATACGCCCTAGAACAGAACCTCCATCAAAGCCATCCCTGCA
 GGAGCCTTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAACATCAGATATCGGA
 TATTGCTCCAGATGCCCTCAGGGCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA
 AGATCACCAGAGATTCCAAGGGACTGTTGATGGCTGGTCTCCTACAGCTGCTCCTCCTC
 AATGCCAACAAAGATCAACTGCCCTGCGGGTGAACACGTTCAAGGACCTGCAGAACCTCAACTT
 GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGCTCTCGCCCCCTGCACT
 CCATCCAGACACTCCACTTAGCCAAAACCCATTGTGTGCACTGCCACTTGAAAGTGGCTG
 GCCGACTACCTCCAGGACAACCCATCGAGACAAGCGGGCCGCTGCAGCAGCCCGCG
 ACTCGCCAACAAGCGCATGCCAGATCAAGAGCAAGAACGTTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTCAGCAGCGAGTGCTCATGGACCTCGTGTGCCCCAGAACGTTGCG
 TGTGAGGGCACGATTGGACTGCTCCAACCAGAACGCTGGTCCGATCCCAAGCCACCTCCC
 TGAATATGTCACCGACCTGCACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCAACCTGCGAAAATAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT
 GGAGACCGTGCACGGCGCGTCTCCGTCAGTGGCCTCAAAACCTGATGCTGAGGA
 GTAACCTGATCAGCTGTGAGTAATGACACCTTGCCGGCTGAGTTGGTCAAGACTGCTG
 TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCTTCACCACGCTGTCTCCCT
 GTCCACCATAAACCTCCTGTCACCCCTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
 AGTGGTTGAGGAAGAGGGCGGATCGTCAGTGGAAACCTAGGTGCCAGAACCCATTTCCTC
 AAGGAGATTCCCATCCAGGATGTGGCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCCGCGCTGCCGGAGCAGTGACCTGTATGGAGACAGTGGTGCAT
 GCAGCAACAAGGGCTCCGCGCCCTCCCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC
 CTGGAAGGAAACCACCTAACAGCGTGCCTGCCAGAGAGCTGTCGCCCTCCGACACCTGACGCT
 TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
 ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCAGCCTTCAAC
 GGGCTGCGGCTCCGTGCGAGTGCTAACCCATGGCAATGACATTCCAGCGTTCCGTGAAGG
 CTCCTCAACGACCTCACATCTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG
 ACTGCAGTCTCGGTGGCTGCGAGTGGGTGAAGGCAGGCTCCTGCTCACCAACCCAAACCGCTT
 CGCTGCAGTAGCCCTGAGCCATGGCTGACAGGCTCCTGCTCACCAACCCAAACCGCTT
 CCAGTGCAAAGGGCAGTGGACATCAACATTGTGGCAAATGCAATGCCCTGCCTCTCCAGCC
 CGTGCAAGAATAACGGGACATGCACCCAGGACCCCTGTGGAGCTGTACCGCTGTGCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTCAGCTGCTCCTGCCCTC
 TGGGCTTGAGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
 AACAAATGCCACCTGCGTGGACGGGATCAACAACATACGTGTATCTGTCCGCCCTAACTACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCAGCTGAACCTCTGTACAGCATG
 AGGCCAAGTGCATCCCCCTGGACAAAGGATTCACTGCGAGTGTGTCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGGCCCACAAGTGCCGCCACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCTGGGCTTCAGTGGACCCCTGTG
 AACACCCCCCACCCATGGTCTACTGCAGACCCAGGCCATGCGACCAGTACCGAGTGCCAGAAC
 GGGGCCAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGCTGCCACCAGGCTCGCCGG
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGCAAAGACTCCTACGTGGAACACTGG
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGCCACTGACAAGGACAAC
 GGCATCCTCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCGAGGCCACGT
 GCAGCTGGTCTATGACAGCCTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTCACAGTGTGGAGCTGGTACGCTAAACCAGACCCCTGAACCTAGTAGTG
 GACAAAGGAACTCCAAAGAGCCTGGGAAGCTCCAGAAGCAGCCAGCAGTGGCATCAACAG
 CCCCCCTCACCTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCCTGGCCAGGGCACGG
 ACCGGCCTCTAGGCCTCCACGGATGCATCCATGAGGTGCGCATCAACAAAGAGCTGCAG
 GACTTCAGGCCCTCCCACCACAGTCCCTGGGGGTGTCACCAGGCTGCAAGTCCTGCACCGT
 GTGCAAGCACGGCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCAGTGCCGCCAG
 GCTGGACCAGGCCACTCTGCAGACCAGGAGGCCGGACCCCTGCTCGGCCACAGATGCCAC
 CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCCTGCTCAGCCTCAAGTGTCAACCATG
 GGCAGTGCCACATCTCAGACCAAGGGAGCCCTACTGCCCTGTGCCAGCCGGCTTAGCGGC
 GAGCACTGCCAACAAAGAGAATCCGTGCCCTGGACAAGTAGTCCGAGAGGTGATCCGCCGCC
 GAAAGGTTATGCATCATGTGCCACAGCCTCAAGGTGCCCATCATGGAATGTGTCGTGGGGCT
 GTGGGCCCTGGCTGCTGCCAGCCCACCCGCAAGCGGCCAGAACATCGTCTTCAGTGCACG
 GACGGCTCCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCCTGCCCTCGCGTGTTC
CTAAGCCCTGCCCTGGTATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
 AGAGAATATTAAGTATATTGTAACAAAAAATAGAACTTAAAAAAAAAAAAAAA
 AAAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFAGLK NLRVLHLEDNQSVIERGAFQDLKOLERLRLNKNKLQVL
 PELLFQSTPKLTRLSENQI QGIPRKA FRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRILVTSFNHMPKIRTIRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVC PAPHEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAI PAGAFTQYKKLK RIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK
 GLFDGLVSLQ LLLL NANKINCLRVNTFQDLQNLNLLS LYDNKLQTISKGLFAPLQSIQTLHL
 AQNP FVCDCHLKW LADYLQDNPIETSGARCSSP RRLANKRISQIKSKKFRC SGS EDYRSRFS
 SEC FM DLV CPE KCRCE GTIVDCSNQKL VRI PSHLPEYVTD LRLNDNEVS VLEATGI FK KLPN
 LRK INL SNNK I KEVREGA FDGA ASVQ EMLTGNQ LETV HGRVFR GLS GLKTLM LRSNL ISCV
 SNDT FAGLSSVRLLS LYDNR ITT IT P GAF TTVSL STINLLS NPNC NC HLA WL GKWL RKRR
 IVSGN PRCQ KPF FLKEI PIQD VAIQ DFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR
 AL PRGMPKDVT ELYLEG NHLT AVPRELSALRH LTIDLSNNSISMLTN YTFSNM SHLSTLIL
 SYNRLRCIPVHAFNGLRS LRVLT LH GNDI SSVPEGSFNDL TSLSHL ALGTNPLHCDCSR WL
 SEWVKAGYKEPGI ARCSSPEPMADRLLTT PTHR FQCKGPVDINIVAKCNACLSSPCKNNGT
 CTQDPVELYRCACP SYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR
 CEINPDDCEDND CENNATCVDG INNYVCICPPNYT GELCDEV IDHCVPELNLCQHEAKC I PL
 DKGF SCECVPGYSGKLCETDNDDCVAHKCRHGAQCVD TINGYTC T CPQGFSGPFC EH PPPMV
 LLQTSPCDQYECQNGAQCIVQQEPTCRCPPGFAGPRCEKLITVN FVGKDSY VELASAKV RP
 QANISLQVATDKDNGILLYKGDN DPLALELYQGHVRLVYDSLSSPTTVYS VETVNDGQFHS
 VELVTLNQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGI PTSTGLS ALRQGT DRPLGGF
 HGC IHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEH CQQENPCLGQVVREVI RQGYASCATASKV PIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCTGAGCTGCCTGTACCGACTAGGTGGAGCAGTGTTCCTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTCAGTTCTGTCT
CCGGCAGGCTTGAGGATGAAGGCTGCCATTCTGACCCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACGGAAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGCCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGCCTGGATGACGGCAGCAGTCAGCTATGGCATCTCCAGATCA
ACAGCTCGCGTGGTGCAGACCGGAAAGCTGAAGGAGAACACCAGTGCATGTCGCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACATTGGCAAGGCTGGAAGAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTCCTAAACTGGAACTGGACCCAGGATGCTTGCAGCAAC
GCCCTAGGATTGCAGTGAATGTCAAATGCCGTGTCACTTGTCCCCTTCCATA
TTCCTTCTCAAACCTGGAGAGGGAAAATTAGCTATACTTTAAGAAAATAATATTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLLIGCLVTGAESKIIYTRCKLAKIFSRAGLDNWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCVAWSALITDDLTDAAIICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

FIGURE 115

CAGGCCATTGCATCCCACTGTCCTTGTGGAGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCTATTAAAACTTGTACATGGCTCCC
 CATTGGTTTGGAGAAAAGTTCAAGCTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACTTCCCAGATCTGCTCTCAC
 CAAGAGAGATTCTTCTAAACGACTATAACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTCACAGCTGCTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCTGATGTCCTCTATCCATCTCTAAATGTCACCAG
 CTTTGACTCAGTTGTCCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATCCTGC
 TGCTCTCCATCAACAGATAACGAAAGGAAGAAAAATCTGACTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAAGATTGACATCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCCCTCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCAGTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCTAGTCATTGCTGTTAACCGCTGGAGT
 CCATTGACCACAGTGTACAGGGTTCTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTCCTAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAATTTCCCTGAAGCATTACAGAACAGCTTACCGATATGTTACCAAAC
 TGCTGGTA**TAA**TCAGATTGTTTAAGATCTCCATTAATGTCATTTATGGATTGTAGACC
 CAGTTTGAAACCAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTAAAAAATAAA
 CTTGAGTCTGAATGTGAGCCACTTCCCTATATACCACACCTCCCTGCCACTTTCAGAAA
 AACCATGTCTTATGCTATAATCATTCAAATTGCTAGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTCAGCAGAGTATTTAATTATTTCTGGGATTATTGCTCTGTCTA
 TAAATTGAAATGATACTGTCCTAATTGGTTTCAAGTTAAGTGTATCATTATCAA
 AGTTGATTAATTGGCTTCAGTATAATGAGAGCAGGGCTATTGTAGTTCCAGATTCAAT
 CCACCGAAGTGTTCAGTCATCTGTTAGGAAATTGCTCTGTCTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTAAGATAATTGTATTTGCACACTGAGATATAA
 TAAAAGGTGTTATCATAAAAAAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFRILARRKKILFYCHFPDLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAASFKEFKSLSHIDPDVLYPSLNVTSDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRILTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIKEFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCA**ACTGAAGAAAAAGATGGTAATCTTCCAGATATT**
 GTGAATAGTGGAAAGTTGCATGAGTCCTGGTTAATTGCATGAGAGATATGGGCCTGTGGT
 CTCCTCTGGTTGGCAGGCCCTCGTGGTAGTTGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCAATAAGACATCGGACCCCTTGAAACCAGTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTGCCCTCCTAAAGCTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTGGTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGTAGTACATTGAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAACATGGCACAGTTGGTCTGAGATTGGAAAAGGCTTCTAGATGGTCAC
 TTGATAAAAACATGACTCGGAAAAAACAAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAACAGACTATGATATTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGCAATCTGTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTGGAAATGGCCTGTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTGAACTGCCA
 AACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTATTATT
 CCTAGAGAGACCCTCGTCCTTATGCCCTGGTGTGGTACTTCAGGATCCTAATACTGGCC
 ATCTCCACACAAGTTGATCCAGATCGGTTGATGATGAATTGAAACTTTCTCTGG
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGTGGAGGGACAGGTTATTGA
 AACAAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTGGATCACTGTCTCAAAGAGAT
 ATTTAAAATTTCATACATTAAAATTGTTAAATTGATTGAGGAAAACAACCATTAAAAAA
 AAATCTATGTTGAATCCTTTATAAACCAAGTATCAGTCACTTGTAATATAACACCTATTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGIPTEEKDGNDLPIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDFETMLKSSLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQE VIRFQKNHGTWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFS LASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDDELVMKT FSSLGFSGTQECPELRFAYMVT TVLLS VLV KRL HLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTCGGCTTGCAGGGAGACTTCAGGAGTCGCTGTCTGAACCTCCAGCCTCAGA
GACCGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTATCACCTATTCTGGTCCCAGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGGAGTATGACAAGCAGGACATTAGCTGG
TGGCCGCGCTCTGTCACCCCTGGCCTCTTGCACTGGAGCTGGCCGGTTCTCAGGA
GTCTCCATGTTAACAGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCCTTCATATTGAGCGTTGGAGTGCACTACGTATTGGTACATTGGTCT
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTATTGTCACCGTCTTGGCTGAAA
AAGAAACCCCTTCTGATTACCTTCATGACGGAACCTAACGGACGAAGCCTACAGGGCAAGGG
CCGCTTCGTATTCCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTCCCCTCGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTAGTGGATTATCCGCATTGTATTAA
GTGCTTGTAAATAAAATGTTTAGTAACATTAAGACTTATACAGTTAGGGGACA
ATTAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFC SALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCCGGACCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGCTAC
AACTTCCTGATTGGAGAACGACGGGCTCGTATACGAGGGCCGTGGCTGGAACTTCACGGGTGC
CCACTCAGGTCACTTATGGAACCCATGTCCATTGGCATCAGCTTATGGCAACTACATGG
ATCGGGTGCCACACCCCAGGCCATCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGA**GGCC
CTGCTGATCCGCACCCATTCCCTCCCATGGCAAAAACCCACTGTCTCCTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTILGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTILGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCAGGGAGGAAGATGCACT
 GACTCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGCCAGG
 ATGATGGTCCTCCCGCTCAGAGGACCTGAGCGTGTGACCACAGGGCCAGCCCCGGCCC
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAACGTCAGTCCCAGGGCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCCTGGGAGGCTTGGGCATTCTTGGCAGCCCCCAACCGCC
 CGAACACAGCCCCCACCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTCCCCCCCAGTAAAGCTGTAGAGTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGAGAAGGTAGAACGGGCCGCCGGACCTC
 GCTTGACCCACGACCCAGCCAAGATCTGCTCCAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCCAGCCCTCAAAGTCGTCTGTGTCTACATGCCCTTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATAACCCCTACTACCCATC
 TGGGTGACCCAGGGCAGGCCACAGAGGCCAGGGCTGGAAGGACAGGCCTGCCATGC
 AGGAGACCATCTGGACACCAGGGCAGGGAAAGGGTTGGCCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGCCAGGGCAAGTCTCAAGTGGCAGAGAAAAGGGTCCAAGTG
 CTGGTCCAAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCAGGGAGGAGTGGCT
 CTCTGTGCAGCCTCACAGGGCTTGCCACGGAGCCACAGAGAGATGCTGGTCCCCGAGGCC
 TGTGGCAGGCCGATCAGTGTGGCCCAGATCAAGTCATGGAGGAAGCTAACGCCCTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGCGCCCTGAGCCCTTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTCCAAAATCCCTTCTGCCAGTACTCCCCCTGTACCAACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAACAGGACGATTGTGGCCTCCACACTAACGCC
 ACAGCCCACCCATCCCGTGCTGTGTCCCTTCCACCCCAACCCCTGCTGGCTCCTGGGAG
 CATCCATGTCCCAGGGAGAGGGTCCCTAACAGTCAGCCTCACCTGTCAGACCCGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGGCGCAGA
 GCATGTGCTGGATCTGTTCTGTGTCTGTGCTGGGTGGGGAGGGAGGGAAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTGTGAAGAATCGTGTCTTGAGCAGGAAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSILVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVANLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKCPDNYHSDTPY
YPSG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTGATGACTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTGGCGCGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTAAAG
 GACAAAGGTAAACAGAGCCAGCGAGAGAGCTCGAGGGAGACTTGACTTCAAGCCACAGAAT
 TGGTGGAAAGTGTGCGCGCCGCCGCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCAGCACCAGGATCCCGGGTAGGAGGCAGCGGGGAGCACCAGGCCAGCC
 GGCTCGGGCTGCCACACGGCTCACATGGGCTCCGGCGCCGGCGCTGTCGCGGTGCCG
 GCCGTGCTGCTGGTCTCACGCTGCCGGGCTGCCGTCTGGGACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGCAGTCGAACCCGGCACGGACTCCAAGG
 GCTCCTCTCCTCCCCGCTGGGATATCGGTCCGGCGGCCACTCCAAGGTGCGCCTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCTTACTT
 CGATCAGATCCTGGTGAATGTGGTAATTTTACATGGAGTCTGTCTTGTAGCACCAA
 GAAAAGGAATTTACAGTTTACGTAAAGTCTACAGAGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACAGTAATATCTGCCTTGCGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGCCTGCTCACCTAGATAAAGAGGATAAGGTTACCTAA
 AACTGGAGAAAGGTAAATTGGTGGAGGCTGGCAGTATTCCACGTTCTGGCTTCTGGT
 TTCCCCCTATAGGATTCAATTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTCATCATTGGATTGATGTCCTTATTGGTTCTCATGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAATTCACAGATTATTGTG
 TGTGTCTGTTCAAGTATATTGGATTGGACTCTAAGCAGATAATACCTATGCTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCATTCCTGGATTACTGAATTAGT
 TACAGATGTGGAATTATTGGATTGTTAGTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAAACTCTAAAGTTCTGACTTCAATCACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATTTGTTTATTCCCTTGGATTAGTTGTTGGTTCTGTAA
 AAAACTGGATTTTTCAGTAACTGGTATTATGTTCTCTAAATAAGGTAAATGAA
 TGGCTTGCCCACAAATTACCTTGACTACGATATCATCGACATGACTCTCTCAAAAAAAA
 GAATGCTTCATAGTTGATTAAATTGTATATGTGAAAGAGTCATATTCCAAGTTATATT
 TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAGTTGCTTACCCAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCGAGGGAAATCTTACTTATTG
 TCAACTTAAATTAAATGATTGATAATAACCACCTTATTAAAAACCTAAGGTTTTTT
 TCCGTAGACATGACCACTTATTAAACTGGTGGGGATGCTGTTCTAATTACCTAT
 TTTCAAGGCTCTGTTGATTGAAGTATCATCTGGTTGCCTTAACCTTAAATTGTA
 TATATTATCTGTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTAGTGAATAT
 CTTGTCTTGTATAGGTATATGAATTCAAAATTATTATGCTGTTAGAATAAAGA
 TTAATATATGTTAAAAAAA

FIGURE 126

MGSGRRALSAVPAVLLVLTLGPLPVWAQNDTEPIVLEGKCLVVCDSPATDSKGSSSPLGI
SVRAANSKVAFAFSAVRSTNHEPSEMSNKTRIIYFDQILVNNGNFFTLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNLMNLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

FIGURE 127

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTCGGCTGCGCCTTCATTGCCTCGGGCCTGCGCTC
GCCCTTATGTCTTACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCCGGAGC
TTTCTTCTGGTTGGTGTCTACTGATTCGTCCTGTTGGTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTGGAGCGTTGTCTGTCTGTC
TATATCCAAGAAATGTTCCGATTGCATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTCTGGCT
TGGGCTTGGAATCATGAGTGGAGTATTTCTTGTGAATACCCATCTGACTCCTGGGG
CCAGGCACAGTGGGCATTCATGGAGATTCTCCTCAATTCTCCTTATTCACTTGTGAC
GCTGGTCATTATCTGCTGCATGTATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGA
AAAAGTGGGCATCCTCCTATCGTTCTCCTGACCCACCTGCTGGTGTAGCCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTATGGCAC
CTGGGCATTCTTAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTCTTACAACCAGCGCTCCAGA**TAA**CCTCAGGGACCAGCACTCCCAA
ACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCTTTCTGAAAATCCCTTTCTG
GTGGAATTGAGAAAGAAATAAAACTATGCAGATA

FIGURE 128

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pi: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKW
GILLIVLLTHLLVSAQTFI SYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKN
FLLYNQRSR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC **ATG**TTCGCTCTGGCTTGCCTTCT
 TGGTGCCTTGGTGGCCTCGGTGAGAGCCATCTGGGGTCTGGGGCCAAGAACGTCTCGCAGAAAGACGCC
 AGTTTGAGGCCACCTACGTGGACGAGGTCAACAGCGACCTGGTCAACATCTACACCTTCACCATACTGTGACCC
 GCAACAGGACAGAGGGCGTGCCTGCTGAACAGTCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTGTGG
 TCCGCCAGAAGGAGGCTGTGGTCTTCCAGGTGCCCTTAATCTCGCAGGGATGTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGAACGAACCTGTGTCAAGCCCCCACCAGAACATGAGTCGGAGATTCAAGTCTTCTACGTGGATG
 TGTCCACCTGTCAACAGTCAACACCACATACCAAGCTCCGGTCAGCCGATGGACGATTGTGCTCAGGACTG
 GGGAGCAGTTCAGCTCAATACCAACAGCACAGCAGCACAGCCCAGTACTTCAGTATGAGTTCCCTGAAGGCCTGGACT
 CGGTAAATTGTCAGGTGACCTCCAAACAAGGCCTTCCCCTGCTCAGTCATCTCATTAGGATGTGCTGTCCTG
 TCTATGACCTGGACAACAACGTAGCCTTCATCGCATGTACAGACGATGACCAAGAAGGGCCATACCGTAC
 AGCGCAAAGACTTCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCCGGGCT
 CCCTGCCCTTCTACCCCTCGCAGAAGATGAACCGTCATCAAGGGCACCGCAGAAAACCCCTGTCAGTGCCTGG
 TGTCTCAAGCAGTCACGCTGAGGCATACGTCAGTGGATGCTCTTGCCTGGTATATTCTCTCCTTTAC
 TGCTGACCCTCCTCCCTGGCCTGCTGGAGAACCTGGAGGAGAAGAAGAACCCCTGCTGGTGGCATTGACCGAG
 CCTGCCAGAAGCGGTACCCCTCGAGTCCTGGTCAATTCTTCCCTGGCAGTTCCCTATGAGGGTTACAAC
 ATGGCTCCTTGAGAATGTTCTGGATCTACCGATGGTCTGGTGAACAGCGCTGGCACTGGGACCTCTTAC
 GTTACCAAGGGCGCTCCCTTGAAACCTGTAGGTAACCTGGGAGACTGGAGGAGTGGACTCCATGAGCTCTGTTGGAGGATG
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCATTGCAACAGAACATACCTCTATGTTGGCTGACC
 TGGCACGGAAGGACAAGCGTGTCTCGGGAAAAAGTACCAAGATCTACTCTGGAACATTGCCACCATTGCTGTCT
 TCTATGCCCTTCTCTGTGGTCAAGCTGGTATCATGTCACCTACAGACGGTGGTGAATGTCACAGGAATCAGGACATCT
 GCTACTACAACATTCTCTGCGCCACCCACTGGCAATCTCAGGCCCTCAACAAACATCCTCAGCAACACTGGG
 ACATCCTGCTGGGCTGCTTCTCTGCTCATCATCCTGCAACAGGGAGATCAACACCAACCCGGGCTGTCGCGCA
 ATGACCTCTGTGCCCTGAAATGTTGGATCCCCAACACTTGGCTTCTACGGCATGGGCACAGCCCTGATGA
 TGGAGGGCTGCTCAGTGCCTGCTATCATGTCATGTCACCTACAAATTCCAGTTGACACATCGTCATG
 ACATGATCGCCGGACTCTGCATGTCAGACGCTTACCAAGCAGGGCACCCGGACATCAACCGCAGCGCCTACAGTG
 CCTACGCCTGCCATTGTCATCTCTCTGTGCTGGCGTGGTCTTGGCAAAGGGAACACGGCGTTCT
 GGATCGTCTTCTCCATTCACATCATGCCACCCCTGCTCCTCAGCACGAGCTCTATTACATGGGCCGGTGG
 AACTGGACTCGGGATCTCCGCCATCTCCACGTGCTCTACACAGACTGCAATCCGGCAGTGCAGCGGGCCG
 TCTACGTGGACCGCATGGTCTGGCATGGCAACGTCATCAACTGGTCTGGCTGCCTATGGCTTATCA
 TGCGCCCAATGATTGCTTCTACTTGGCATCTGCAACCTGCTCTTACTTCGCTTCTACA
 TCATCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCACTGTTGCACCTCCGGTGG
 GGGCTTCGCGCTCTTCTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAAGAGTCAGGGAGCACA
 ACCGGACTGCATCCTCGACTTCTTGACGACCACGACATCTGGCACTTCTCTCCATGCCATGTTG
 GGTCTTCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGCAAGCGGGACAAGATCTATGCTTC **TAGC**
 AGGAGCTGGGCCCTCGCTCACCTCAAGGGCCCTGAGCTCTTGTGTCATAGACGGGTCACTCTGCTGTGCT
 GTGGGGATGAGTCCCAGCACCCTGCCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT
 GGGACAGCCATGGGTGGCATGGAACCTTGCACTGGTCTGCCAGGGAGGAGCAGGCCCTGCTCCCTGGAACCCCC
 AGATGTTGGCAAATTGCTGCTTCTCTCAGTGTGGGGCTTCCATGGGCCCTGCTCTTGGCTCTCCATT
 GTCCCTTGCAGGAGGAAGGATGGAAGGGACACCCCTCCCATACTCCACTCAGGGCTAGTCTGGGGCTGA
 ACAATGCCCGCCTGGGACCTAAGGGCTCTTCCCTCCATACTCCACTCAGGGCTAGTCTGGGGCTGA
 ATCTCTGCTCTGTTAGTCAAGGGCTGAATCAGAGGTCAACCTCTCATCCATCAGCTCCAGACTGATGCC
 AGGATGGATGGGGTATGAGATTGGGGTGGCCAGCTGGTCCAGACTTGTGCTAAGGGCTGCAAGGG
 CCTGGGGCAGTGCCTATTCTCTTCCCTGACCTGTGCTCAGGGCTGGCTCTTAGCAATGCGCTAGCCAAATT
 TGAGAACCGCCTCTGATTCAAGGGCTGAATCAGAGGTCAACCTCTCATCCATCAGCTCCAGACTGATGCC
 AGCACCAGGACTGGAGGGAGAAGGCCCTACCCCTCCCTTCCAGGCCCTAGTCTTGGCAGGCTAGTCTGCC
 AGCTGGTGGCCTTCAGTGCCTTGCACACTGCCAAGAACATGTCAGGGCAAAGGGAGGGATGATACAGAGTT
 CCCGTTCTGCCCTCACAGCTGTGGCACCCAGTGCCTACCTTAGAAAGGGCTCAGGAAGGGATGTGCTGTT
 CCCTCTACGTGCCAGTCTAGCCTCTAGGACCCAGGGCTGGCTCTAAGTTCCGCTCAGTCTCAGGCA
 AGTCTGTGTTAGTCATGCACACACATACCTATGAAACCTGGAGTTACAAAGAATTGCCCAAGCTCTGGG
 CCTGGCCACCTGGTCTGGATCCCCCTCGTCCACCTGGTCCACCCAGATGCTGAGGATGGGGAGCTCAGG
 CGGGGCTCTGCTTGGGATGGGAATGTTTTCTCCAAACTTGTGTTTATAGCTCTGCTTGAAGGGCTGG
 AGATGAGGTGGGTCTGGATCTTCTCAGAGCGTCTCCATGCTATGGTGCATTCCGTTATGAATGAATT
 TGCATTCAATAAACACCAACTCAAAAAAAAAAAAAA

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pi: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNNTYQLRVSRMDDFVLRTGEQFSFNTAAQPQYFKYEFPSEGVDVSI
VKVTSNKAFPCSVISIQDVLCPVYDLDNNVAFIGMYQTMTKKAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVQDQGHRQKTLSQLSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACPESGHPRVLADSFPGSSPYEGYNFGSFENVSGSTDGL
VDSAGTGDLISGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLDIDSCKNVRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYIILLGLLFLLIILQREINHNRAALLRNDLCALECGIPKHGLFYAMGTALM
MEGLLSACYHVCNPNTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIIIIATLLLSTQLYYMGRWKLDSGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSIAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRDCIILDFDDHDIWHLSSIA
MFGSFLVLLTLDDDDTVQRDKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCTGCCCTGCCCAACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGCGCTGGAGGGCTGTCTG
 ACC**ATG**TCCCTGCCTGGCTGTGGCTTGTGTCTCCGCCCCAGGTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTGTGAAGTCCAGAAAATATGGTGGAAATTTCCTTATACC
 TGACCAAGTTGCCGCTGCCCGTGAGGGGGCTGAAGGCCAGATCGTGTCTGAGGGACTCA
 GGCAGGCAACTGAGGGCCCATTGCTATGGATCCAGATTCTGGCTTCTGCTGGTACCCAG
 GGCCTGGACCGAGAGGAGCAGGAGCAGTACAGCTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
 CCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGTACAGGCCTGGCATCCC
 CTCCTCTCCTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACCTGGATCTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGCTCTGCCCTCAGCCCCAAGGGAGCACCGCCTGACCACGCCCTGGAGAGGAC
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCTAGGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCTATAACCCGACACATGGCCAGGTACACTGGAGTGGGGTGTGATGT
 GCACTATCACCTGGAGAGCCATCCCCCGGGACCTTGAAGTGAATGCAGAGGAAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAACGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCCATGGCGAGGAGCATGCGCCCTCTGGAGCTGCACGTGCTGGTATGGATGAGAA
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGAAGTACTGAGCTGTCAGCAGAGGATGCAGATGCCCGGCTCCCCAATTCC
 CACGTTGTGTATCAGCTCTGAGCCCTGAGCCTGAGGATGGGTAGAGGGAGAGCCTTCCA
 GGTGGACCCCACCTCAGGCAGTGTGACGCTGGGGGTGCTCCACTCGAGCAGGCCAGAACAA
 TCCTGCTCTGGTGCCTGGCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
 GAAGTCGAAGTCGCACTGACAGATATCAATGATCACGCCCTGAGTTCATCACTCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGGCCGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCGCTTCGCCTCATGGATTTGCCATTGAGAGGGAGACACA
 GAAGGGACTTTGGCCTGGATTGGGAGCCAGACTCTGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGCAGAGTGTGGCGA
 AGCTGGTGGGCCAGGCCAGGCCCTGGAGCCACGCCACGGTACTGAGGCCAGTGTCCCCATCAGTGC
 AGCCGGCTTTCCCTGCTGACCATCCAGCCTCCGACCCATCAGCGAACCTCAGGTTCT
 CCCTAGTCATGACTCAGAGGGCTGGCTCGCATTGAGAAATTCTCCGGGAGGTGCACACC
 GCCCAGTCCTGCAGGGCGCCAGCCTGGGACACCTACACGGTCTGTGGAGGCCAGGA
 TACAGCCCTGACTCTGCCCTGTGCCCTCCAAATACCTCTGCACACCCGCCAAGACCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGCACGGTCCCTACAGC
 TTCACCCCTGGTCCAACCCACGGTGCACAGGGATTGGCGCCTCCAGACTCTCAATGGTTC
 CCATGCCTACCTCACCTGGCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCTGGTTGAGTGTGTCGCTGCAAC
 GTGGAGGGCAGTGCATGCGAAGGTGGCCGCATGAAGGGCATGCCACGAAGCTGTC
 AGTGGGCATCCTGTAGGCACCCCTGGTAGCAATAGGAATCTCCTCATCCTCATTTCA
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGC
 ACTGTC**TGA**ATGGCCCAGGCAGCTAGCTGGAGCTGGCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGGCCAGCACCAAGATCCAGCAGGGACAGGACAGAGTAGAAGCCCTCCAT
 CTGCCCTGGGGTGGAGGCACCATCACCACGCCAGGATGTCTGCAGAGCCTGGACACCAAC
 TTTATGGACTGCCCATGGAGTGCTCAAATGTCAGGGTGTGTTGCCAATAATAAGCCCCA
 GAGAACTGGCTGGCCCTATGGGAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQAQEYQLQVTLEMQDGHVLWGPQPVLVHKDENDQVP
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRL
GALALSPKGSTS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSI IESTWVSLEPIHLAE
NLKVLYPHHMAQVHWSGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN
SHGEDYAAPLELHVLMVDENDNVPICPPRDPTVSIPELSSPPGTEVTRLSAEDADAPGSPNSH
VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVPLRAGQNI LLV LAMDLAGAEGGFSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRLMDFAIERGDTE
GTFGLDWEPDSGHVRLRLCKNLSYEAAAPSHEVVVVVQSVAKLVGPGPGATATVTVLVERV
MPPP KLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWL CIEKFSGEVHTA
QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
TLGP NPTVQRDWRLQTLNGSHAYLT LALHWVEPREHIIPVVVSHNAQM WQLLVRVIVCRCNV
EGQCMRKVGGRMKGMPTKLSAVGILVGT LVAIGIFLILIFTWTMSRKKDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGAC**ATG**AGGTGGATACTGTTATTGGGCCATTGGGTCCAGCATCTGGCCAA
 GAAAAATTGGGGACCAAGTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAAAGTAGTGAATTCAAACAACCTGAAGCTCAATTCTGGAAATCTCCCTCCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCAGTCTGCAGGCATTAAATCCTCCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACCTCAACTACGGGG
 CTTACCATCCCTGGAAGCTATTACACAGAGATGGACAACATTGCCAGACTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTGTTGAAAACCAGGCCATGTATGTACTGAAGTT
 CAGCACTGGGAAAGCGTGAGGCAGGCCGTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAAGGG
 GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTCTTCTGTTGCCGTGGCCAATCC
 TGATGGATATGTGTACTCAAACCTCAAACCGATTATGGAGGAAGACGCCGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGCCTGACCCAAATAGAAACTGGAACGCTAGTTGCAAGGAAAG
 GGAGCCAGCGACAACCTTGCTCCGAAGTGTACCATGGACCCCAGCCAATCGGAAGTGGA
 GGTGAAATCAGTGGTAGATTTCATCCCCAACATGGGAATTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGCAGCTGCTGATGATCCATATGGTACTCAGTCAAAAGGCCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTGCGGCCAAAGCTCTGGCTCTGTGTCGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAACGGCATCAAATTGCAATTGAGTTGAGAGATACCGGGACCTATGGC
 TTCCCTCTGCCAGCTAACCAAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGCTGAAGAC
 CATCATGGAGCATGTGCGGACAACCTCTACT**TAG**GCGATGGCTCTGCTCTGTCTACATTAT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTTTCTACCTGTGAG
 TCAGAGCCCTCTGGTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTCTGGCGTGTCCCTGCAAGAACTGGTCTGCCAGCCTGCTCAATTGGTCTG
 CTGTTTTGATGAGCCTTTGTCTGTTCTCCCTCCACCTGCTGGCTGGCGGCTGCACTC
 ACCATCACCCCTCCTGGTGGCATGTCTCTCTACCTCATTAGAACCAAAGAACATC
 TGAGATGATTCTTACCCATCTAGCCAAGCCAGTGCACCTGCTCTGGTGGCACT
 GTGGGAGACACCAACTGTCTTAGGTGGTCTCAAAGATGATGAGTAAATTCTTAATTTC
 TCGCAGTCTCCTGGAAAATATTCTTGTGAGCAGCAAATCTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCCCTGTTTTGGAGACAGAGTTGCTCTGGTCTGTTGCC
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTACCACAAACCTCTGCCCTGGTTCAAGCA
 ATTCTCCTGCCTCAGCCTCTGAGTAGCTGGTTTATAGGCAGCATGCCACCATGCCCTGGCTA
 ATTTGTGTTTAGTAGAGACAGGGTTCTCCATGTTGGCTAGGCTGGCTCAAACCTCCCA
 ACCTCAGGTGATCTGCCCTCCTGGCCTCCCAGAGTGTGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCGTCCCTCTTTAGGCCTGAATACAAAGTAGAGATCATTCTTAC
 TGTGCTGAGAATTCTAGATACTCAGTTACTCCTCTCCCTTGTATTCAAGTGTG
 ACCAGGATGGCGGGAGGGATCTGTGCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCACCTAAATGCAGGATGGTCAAATTACCCATCTGCTCTAATGGGCTTACCTCCT
 CTTGCCTTTGAACACTCAAAGATCTAGGCCTCATCTTACAGGTCTAAATCACTCAT
 CTGGCCTGGATAACTCACTGCCCTGGCACATTCCATTGTCAGGCTGGTGTGTT
 TCTGTCTATTGTATCCTGGACCAAGTCTAAAGTAGAGCAAGAATTCAACCAGCT
 GCCCTCTGTTTACAAACATGTCTGAAATCTTAACCTCCTGCCCTAGGATTGTACA
 GCATCTGGTGTGCTTATAAGCCAATAATTCAATGTGAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFQGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDEMHQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKVRRPAVWLNA
GIHSREWI
SQATAIW TARKIVSDYQRDPAIT SILEKMDIFLLPVANPDGYVYTQTQNLWRKTRSRNPGS
SCI GADPNRNWNAS FAGKGASDN PCSEVYHGPHANSEVEVKS VVDFI QKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLA
AKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQI IPTAEETWLGLKTIMEHVRDNLY

Signal peptide:

amino acids 1-16

FIGURE 135

FIGURE 136

MASYLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFPVSVSTSLAMILGAHSVTKTQILQGLGFNLHTHPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELOLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK
VVDDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDAVAFFVLPKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGC
 CTGAGTCCAAGATTCTCCCAGGAACACAAACGTAGGAGACCCACGCTCTGGAAGCACCAG
 CCTTATCTCTCACCTCAAGTCCCCTTCTCAAGAATCCTCTGTTCTTGCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTGCTTCCAGCCACAAAGAGACAG**ATG**AAGATGC
 AGAAAGGAAATGTTCTCCTTATGTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
 CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCA
 GCGTGACCTCCAATGGGGTCAGCATAGTCACCAACTCTGAGTCCATACAACCTCCAGTGGG
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA
 CTCTGAGTCCAGCACAACTCCAGTGGGCCAGCACGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGCCAGCACAGTCACCAACTCTGGTCCAGTGTGACCTCCAGTGGAGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA
 GTCTAGCACACTCTCCAGTGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCTCCA
 GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGCCAGCACAGCC
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG
 CACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGG
 CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCCAGCACAGCCACCAAC
 TCTGACTCCAGCACAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC
 CTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCTAGCA
 CAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAG
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCCAG
 TGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCCA
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAGTCCAGC
 ACAACCTCCAGTGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGG
 TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGCCAGCACAGCCACCAACT
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAAAC
 TCCAGTGGGCCAACACAGCCACCAACTCTGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC
 AGCAGCTCTGACTGGAATGCACACAACCTCCATAGTCATCTACTGCAGTGAGTGAGGCAA
 AGCCTGGTGGTCCCTGGTGGCGTGGAAATCTCCTCATCACCCCTGGTCTGGTTGTGGCG
 GCCGTGGGCTCTTGCTGGCTCTTCTGTGAGAAACAGCCTGTCCTGAGAAACAC
 CTTAACACAGCTGTCTACCACCCATGGCCTCAACCAGGCCCTGGTCCAGGCCCTGGAG
 GGAATCATGGAGCCCCACAGGCCAGGTGGAGTCCTAACTGGTTCTGGAGGAGACAGTA
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCC**TGA**GCAGCCCCGGAAAGCAAG
 TGCCGCATTCTCAGGAAGGAAGAGACACTGGCACCCAAAGACCTGGTTCTTCTTCATTCTAC
 CCAGGAGACCCCTCCCAGCTTGTGAGATCCTGAAAATCTGAGAAAGGTATTCTCACC
 TTCTGCCTTACAGACACTGGAAAGAGAAATACTATATTGCTCATTAGCTAAGAAATAA
 ATACATCTCATCTAACACACACGACAAAGAGAAAGCTGTGCTTGCCTGGGGTGGGTATCTAG
 CTCTGAGATGAACTCAGTTAGGAGAAACCTCCATGCTGGACTCCATGGCATTCAAAA
 TCTCCACAGTAAAATCCAAAGACCTCAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 138

MKMQGNVLLMFGLLHLEATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVTSNGSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS
GASTATNDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTTSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGAPHRPRWSPNWFWRPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAAATAGCAGCGTGGCTCCCTGGCTCCTCTGCATCCTCCGACCTTC
CCAGCAATATGCATCTGCACGTCTGGCGGCCCTGCTCCCTCTGCTACTGGGGGCC
CTGTCTGGATGGCGGCCAGCGATGACCCATTGAGAAGGTATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATCAACAGTGGATCACGC
ATGCCGGAAGGGAAAGTGGAGAAGGTTCAACGGACTTAGCAACATGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCCTCCAGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGTCAACAAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTCCACACTGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATATAATGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCACACGCCCTTCATCAACCTTCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCTAAACTGGCATCCGGCTTGCTGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
ATGACCTGGAGGGTTGGGGGACAGGTTCTGAAATCCCTGAAGGGGGTTGACTGG
GGATTTGTGAATAAAACTTGATACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pi: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHAAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGCGGCCCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
 CCCGCGGGGGCGATGACCGTGCGTGAACCTGACTCACTCCAGTCCGGAGGCAGGGGGCCCCCGGGCGACTCG
 GGGCAGCCGGGGCGGAGCTGCCGCCGTGAGTCCGGCGAGCCACCTGAGCCCAGGCCGGACACCGTC
 GCTCCTGCTCTCGA**ATG**CTGCGCACCGCATGGGCTGAGGAGCTGGCTGCCGCCCATGGGCGCCTGCG
 CCTCGGCCACCGCTGCTGCTCTGCTGCTGCTGCCCTGCTGAGCCGCCCTCCGACCTGGGCGCTCAGC
 CCCCCGATCAGCCTGCCCTGGGCTCTGAAGAGCGGCCATTCCCTAGATTGAAGCTGAACACATCTCAACTAC
 ACAGCCCTCTGCTGAGCAGGGATGGCAGGGACCTGTACGTGGGTGCTCGAGAGGCCCTTTGCACTCAGTAGC
 AACCTCAGCTCCTGCCAGGCGGGAGTACCAAGGAGCTGCTTGGGCTGAGACGCAGAGAAACAGCAGTGC
 AGCTTAAGGGCAAGGACCCACAGCGCAGTGTCAAAACTACATCAAGATCCTCCTGCCGCTCAGCGCAGTC
 CTGTTCACCTGTGGCACAGCAGCCTCAGCCCCATGTGTACCTACATCAACATGGAGAACTTCACCCGGCAAGG
 GACGAGAAGGGAAATGTCCTCCTGGAAGATGCAAGGGCGTTGTCCTTCGACCCGAATTCAAGTCCACTGCC
 CTGGTGGTTGATGGCAGGCTCACACTGGAACAGTCAGCAGCTTCAAGGGAAATGACCCGGCCATCTCGCGGAGC
 CAAAGCCTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTGTGGCCTCAGCCTAC
 ATTCTGAGAGCCTGGGAGCTTGAAGGCGATGACAAGATCTACTTTCTTCAGCAGACTGGCAGGAA
 TTTGAGTTCTTGAGAACACCATTGTGTCCCGATTGCCGCATCTGCAAGGGCAGTGGAGGTTGGAGAGCGGGTG
 CTACAGCAGCGCTGGACCTCCTCAAGGCCAGCTGCTGTGCTCACGGCCGACGATGGCTCCCTTCAAC
 GTGCTGAGGATGTCTCACGCTGAGGCCAGGCCAGGACTGGCGTGAACCCCTTTCTATGGGCTTCACT
 TCCCAGTGGCACAGGGAACTACAGAAGGCTCTGCCGTGTTGCTCACAATGAAGGATGTGAGAGACTCTTC
 AGCGGCCTCTACAAGGGGTGAACCGTGAAGCACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCGG
 CCTGGAGCGTGCATCACCAACAGTGGCGGGAAAGGAAGATCAACTCATCCCTGAGCTCCAGACCCAGCGTGTG
 AACTCCTCAAGGACCACTCCTGTATGGACGGCAGGTCAGGCGCATGCTGCTGAGCCCCAGGCTCGC
 TACAGCGCGTGGCTGTACACCGCTCCCTGGCTGCACACACCTACGATGTCCTCTGGGACTGGTAC
 GGCGGCTCCAAGGCAAGGCACTGGCGTCTCGGTGTTGTCACATCATTGAGGAGCTGAGATCTCTCATGGGA
 CAGCCCAGTGCAGAATGTCCTGACACCCACAGGGGCTGCTGATGCGGCTTCACACTGGGCTAGTCCAG
 GTGCCCATGGCCAAGTGCAGCCTGTACCGGAGCTGTGGGACTGCTCCTCGCCGGACCCACTGTGCTTG
 AGCGGCTCCAGCTGCAAGCACGTCAAGCTTACAGCCTCAGCTGGCCACCAGGGCTGGATCCAGGACATCGAG
 GGAGCCAGGCCAAGGACCTTGCAGCGCTTCGGTGTGTCCTCGTCTTGTACCAACAGGGGAGAAGCCA
 TGTGAGCAAGTCCAGTCCAGGCCAACACAGTGAACACTTGGCCTGCCGCTCTCAACACTGGGACCCGA
 CTCTGGCTACGCAACGGGCCCCGTCAATGCCCTGGCCTCTGCCACGTGCTACCAACTGGGACCTGCTGCTG
 GTGGGCAACCAAGCTGGGGAGTCCAGTGTGGTCACTAGAGGAGGGCTTCAGCAGCTGGTAGCCAGCTAC
 TGCCCAGAGGTGGTGGAGGACGGGTGGCAGACCAAACAGATGAGGGTGGCAGTGTACCGTCATTATCAGCACA
 TCGCGTGTGAGTGCACCAAGCTGGTGGCAAGGCCAGTGGGTGCAAGACAGGTCTACTGGAAGGAGTTCTGGT
 ATGTGCACTGCTTTGCTGGCGTGTGCTCCAGTTATTCTGCTTACCGCACCGAACAGCATGAAA
 GTCTTCTGAGCAGGGGAATGTGCCAGCGTGCACCCCAAGACCTGCCCTGTGGTGTGCCCTGAGACCCGC
 CCACTCAACGCCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACAGTCCCTGTCAGACAGCCCCCG
 GGGGCCGAGTCTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTCGTGAGGTATCCCAGTG
 TGCCCCGGCCCCGGCTCCGCTGGAGATCCGTACTCTGGTG**TGA**GAGCTGACTTCCAGAGGACGC
 TGCCCTGGCTCAGGGGCTGTGAATGCTGGAGAGGGTCAACTGGACCTCCCGCTCTGCTTCTGTGGAAAC
 ACGACCGTGGTGGCCGGCTTGGAGGCCAGCTGGCTGCTCCAGTCAGTAGCGAAGCTCC
 TACCAACCCAGACACCCAAACAGCGCTGGGGCAGAGGTCTGGCCAATATGGGGGCTGCTAGGTTGGTGGAA
 CAGTGTCTTATGTAACAGGCCCTTGTAAAAAAACATTCAAATGTGAAACTAGAATGAGAGGGAGAG
 ATAGCATGGCATGCAGCACACACGCGTGTCCAGTTACGCCCTCCAGGGGTGCTGGGAGTCATCAAAGTGG
 TTGCTGAGACAGAGTTGAAACCCTCACCAACTGGCCTCTTCACCTTCACATTATCCCGCTGCCACCGGCTG
 CCTGTCTCACTGCAAGATTAGGACAGCTTGGCTGCGTGTGCTGCCAGTCAGCCGAGGATGTAGTTG
 TTGCTGCCGTGTCCTCCACCACTCAGGGACCAAGGGCTAGGTTGGCACTGCCAGGTCTGGGCTC
 GGACCCAACCTCTGGACCTTCCAGCCTGTATCAGGCTGTTGCCACACGAGAGGACAGCGCAGCTCAGGAGAGA
 TTTCGTGACAATGTACGCCCTTCCCTCAGAATTAGGGAAGAGACTGTGCGCTGCCCTCCGTTGGTGTG
 GAACCCGTGTGCCCTTCCACCATATCCACCCCTCGCTCATTTGAACCTAAACACGAGGAACACTAATGCA
 CTGGTCTCTCCCCAGTCCCCAGTCACCCCTCATCCCTCACCTCCACTCTAAGGGATATCAACACTGCC
 AGCACAGGGGCCCTGAATTATGTGGTTTATACATTAAAGATGCACTTATGTCATTTTAATAAAA
 GTCTGAAGAATTACTGTTAAAAAAAAAA

FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pi: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPLL LLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEGNVLLEDGKGRCP
FDPNFKSTALVVVDGELYTGTVSSFQGNDPAISRSQSLRPTKTESSLNLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETQEFEFFENTIVSRIARIICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFNFNVLQDVFTLSPSPQDWRTTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFILMDGQVR
SRMLLLQPQARYQRVAHVHPGLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSPLYQP
QLATRPWIQDIEGASA KDLCSASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNLATR
LWLRLNGAPVN ASASCHVLPTGDLLL VGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPIIISTSRV SAPAGGKASWGADRSYWK EFLVMCTLFVLAVLLPVLFL YRHRNSM
KVFLKQGECASVHPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLS D SPPGARVFT ESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCCGGCGCCGGCTACGAAGAGGACGGGGACAGGCCGTGCGAACCGA
 GCCCAGCCAGCGGAGGACGCCGGAGGGCAGGGAGGGACGGGACTCGTCTGCCGCCGTGCGCGCTCG
 TGCCGGCCCCCGTCCCCCGCCGGAGCGGGAGGAGCCGCCACCTCGCCTGGCGCCAGGCCGCTAGCGCGCG
 CGGCATGGTCCCCTCTAAAGGCCAGGCCGGCGGGGGCGGGTGTGCGGAACAAAGCGCCGCCGG
 CCTGCCGGCGCTCGGGGCCGATGGCGCCGGGGCCGCGGCCGGCGCTGCCGCCGCTCG
 CGCGCTAGGCCGGCTGGCTCCGTGGCGGGCAGCGGGCTAGGGCGCGAGCGCTGCCGCCGG
 GGCGCGGCCGGCGGCCGGAGCGGCCGGCAT**ATG**GCCGCCGCCGCCGCCCTGGCTAGCGTGC
 TGCTCGGGCTCGTCTGGCTCGTCTGGCTCGCGGCTCGTCTGCCGCCGGCTTCGAGCTGAAGCGAGCG
 GCCCACGGCGCCGCCAGCCCCGAGGGCTGCCGGTCCGGCAGGCCGGCTCCAGGCCGGCGCG
 GCGATGCGCGGGCGAGCTCTGGCCGCCGGCTCGAACCCAGATGGCGGCCGCGACAGGAACCTTCTCT
 TCGTGGGAGTCATGACCCCCAGAAATACCTGCAGACTCGGGCGTGGCCGCTACAGAACATGGTCCAAGACAA
 TTCTGGAAAGTTCAGTTCTCAACTGAGGGTTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGGG
 GTGTGGACGACTCCTACCCGCCAGAAGAACGATCCTTCATGATGCTCAAGTACATGCACGACCAACTTGGACA
 AGTATGAATGGTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACCTCCTGAGGAGTT
 TGAACAGCAGCGAGCCCCCTTTCTGGCAGACAGGCCCTGGCACCGGAAGAAATGGAAAATGGCCCTGG
 AGCCTGGTGAGAACTTCTGCATGGGGGGCCTGGCGTATGAGCCAGGCCATGCCACAACTACAGCTGCACCGCGAAA
 ACATTGGCAAGTGTCTCCGGAGATGTACACCACCATGAGGACGTGGAGGTGGAAGGTGTGCGGAGGTTTG
 CAGGGGTGCAGTGTCTGGCTTATGAGATGCCAGCCTTTTATGAGAACATCGAGCAGAACAAAAGGGGT
 ACATTAGAGATCTCCATAACAGTAAAATTCAACAGCTATCACATTACACCCAAACAAAACCCACCTACCAAGT
 ACAGGCTCCACAGCTACATGCTGAGCCGAAGATATCCGAGCTCCGCCATGCCACAATACAGCTGCACCGCGAAA
 TTGCTCTGATGAGCAAATACAGCAACACAGAAATTCAAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCTCA
 TGAGGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGAGTTCTGACTGGAAAATACTTGATTCGGCAG
 TTGAGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGGGGAAGCCTTGAGCACATTGATGCAGGTCA
 TGGAGATGATCAATGCCAACGCCAACAGCAGAGGGCGCATATTGACTCTCAAAGAGATCCAGTACGGCTACCGCC
 GGGTGAACCCCATGTTAGGGCTGAGTACATCCTGGACCTGCTGCTCTGTACAAAAAGCACAAAGGAAGAAAA
 TGACGGTCCCTGTGAGGAGGCACCGTATTACAGCAGACTTCAGCAAATCTGGATCTTGCTTCTCTCAAACCTCCTGAAGA
 AGCTCGTCCCCCTTCAGCTCCCTGGCTGAAGAGTGAAGCACAAAGAACGATAAAAGATAAACATACTGA
 TTCTTTGCTGGCGTTCGACATGTTGTGAGATTATGGAAACTTGTGAGAACAGCTGTCTTACCCAAATC
 AGAACGTCAAGCTCGTGGTCTGCTTTCAATTCTGACTCCAACCTGACAAGGCCAACAAAGTGAACGTGATGA
 GAGATTACCGCATTAAGTACCCCTAACCGCAGATGCAGATTGCTCTCTGCGACGTCGACCTCGTGTACTA
 CCCTGGAAGTAGGATCCTCCAGTTAACATGAATCTTGCTCTCTGCGACGTCGACCTCGTGTACTA
 CAGAACTCTCAGCGATGTCGAGCAAATACAGTTCTGGCCAACAAATATATTCCAATCATCTCAGCCAGT
 ATGACCCAAAGATTGTTATAGTGGAAAGTCTCCAGTGACAAACCATTTGCCCTTACTCAGAAAATGGCTTCT
 GGAGAAACTATGGTTGGCATCACGTGATTATAAGGGAGATCTGTCGAGTGGTGGCTTGATGTTCCA
 TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTCAACAAAGGTTGTCAGGCCAGGTTGAAGACGTTAGGAGCC
 AGGAAGTAGGAGTAGTCCACGTCCACCATCTGCTTTGTGATCCAATCTGACCCCAACAGTACAAAATGT
 GCTGGGGTCCAAAGCATCGACCTATGGTCCACCCAGCAGCTGGTGAGATGTGGCTGGAAAAAAATGATCCAA
 GTTACAGTAAAGCAGCAATAAAATGGCTCAGTGAGGACAGCC**TAAT**GTCAGCTTGCTGGAAAAGACGTT
 TAATTCTAATTATTTCAAAATTGTTGTGATGAGCTTGTGAGGTTGCTGAGTACCTGCTGAGGATATTTTAC
 AAGTGGTTCTTACATAGGACTCTTAAAGATTGAGCTTCTGAAACAAGAAGGATGTCAGTGTGCTTGT
 CACATCTTCTGCTGAACATTATGTAGCAGACCTGCTTAACCTTGACTGAAATGTACCTGATGAACAAAATTT
 TTTAAAAAAATGTTCTTGTGAGACCCCTTGTGCTCCAGTCTATGGCAGAAAACGTGAACATTCTGCAAAGTAT
 TATTGTAACAAAACACTGTAACTCTGGTAAATGTTGTGATGTTTAACATTCCACAGATTCTACCTTTGT
 GTTTGTTTTTACAATTGTTAAAGCCATTGCTGAGCTGAGTTGATCATTGCTCTCATGGTACTCTGCTCAGCATGGC
 CACGTAGGTTTTGTTGTTGTTGAGACGGAGCTCACTTCAACCTCCACTTCCCTGGTCAAGCAATTCCCTGCC
 CAGTGGCGCAATCTGGCTACTTAAACCTCCACTTCCCTGGTCAAGCAATTCCCTGCCCTTGCCCTCCGAGT
 AGCTGGGATTACAGGCACACACCACGCCAGNTAGTTTTGTATTAGTAGAGACGGGGTTACCAT
 GCAAGCCCAGCTGCCACGTAGGTTAAAGCAAGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
 TGGTAGTTCATCGGCCAAATAGACCTGGCATTAAATTCAAGAAGGATTGCACTTCTCTTGTGACCC
 CTCTTAAAGGGTAAATATTAGTTGAGAACAGATGAATTATTACAATAATCTGATGTACACAGACT
 GAAACATACACACATACACCCCTAATCAAACGTTGGGGAAAATGTTGTTGTTCTTCTCATCCTGTCTG
 TGTATGTGGGGAGATGGTTTCACTCTTCAATTACTGTTGTTTATCCTTGTATCTGAAATACCTTAA
 TTTATTAAATATCTGTTGTTCAAGAGCTCTGCCATTCTGAGTACCTGTTAGTTAGTATTATTATGTATCGG
 GAGTGTGTTAGTCTGTTATTGCAAGAACCGATCTCAAAGATTCTTGGAAACGCTTTCCCTCC

FIGURE 143B

TTAATTTTATATTCTTACTAAATATTAAGTGTCTTGACAATTGGTGCATGTGTTGG
GACAAAAGTGAATGAATCTGTCATTACAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTGTT
TTCATTTAGATTCAAACAGTGATAGACTGCCATTAAATACACGTCATTGGAGGGCTCGTATTGTAAATAG
CCTGATGCTCATGGAAAAATAAACCGAGTGAACAATATTTCTATTGTAATTCAACCATTGTCTCATT
ATTCCCTGTTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAACTAAACACGAAAAAA

FIGURE 144

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pi: 9.52, NX(S/T): 3
MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTI PGKVQFFSSEG
SDTSVPPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDILQLGIPPSFMRFQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLLYKKHKKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSENHFRAFT
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEDVDFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGCAGGACTCCGCTGACACCTTCCC
 TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCCTATGAAGCCTTAGTCCTCTAGTGCCTTGCATGGCCTTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAAACTTGAATCATTATATA
 CAAGTTTAGAGAACCTAGTACGAAGTGTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC
 TAACTCTCCAAAACATGTTATTCTATAGCATCAAAGGGATCAAATTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTAACCAATCCTATCAGTGAAGAAACTACA
 ACTTTCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAAATGTTCCATTGTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGGCCAGGCCAGGCCAGCTGCAAAACAAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCATATGTTACCTCATACAAGTCACCTGTCAC
 CACTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCTCAGCTCT
 CAGGTGAAACTGCGATAGAAAAACCGAAGAGTTGGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTGAAAAAAATTTAGATATTAATTCAAAGTGCAACAGGCACCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
 TTGCTCTAGCAGCAGCAGAACATAAATAAAAACAAATGTATAAGTCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTACATGCTGTGAATTC
 TAGATCTAAACTCTATGAATATTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAAATACATTAAAAATATGTGAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTATTAAACAATAATATAAAATTAAACCTACTGATATTCCATAACAAAGCTGA
 TTTAAGCAAACGTGCAATTTCACAGGAGAAATAATCATATTGTAATTCAAAAGTTGTAT
 AAAAATATTCTATTGTTAGTCAAATGTGCCAACATCTTATGTGTCATGTGTTATGAACA
 ATTTCATATGCACTAAAAACCTAATTAAAATAAAATTGGTCAGGAAAAAA

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLNPISEETTFPTGGFTPEIGKKKTESTPFWSI
KPNNVSIVLHAEPYIENEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPEWNNDDILKKILDINSQQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAEEHKLKTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCACGGCTCCTGCGCCTGAGACAGCTGGCTG
 ACCTCCAAATCATCCATCCACCCCTGCTGTCACTGTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**ATG**GCTTTGTGCTCATTTGGTTCTCAGTTCTACAGAGCTGGTGTAGGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTGTCCAGGCCTGGTGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTCCAGACCAGTGCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGAAGACTGGGAATCTAACAGATGCCACA
 GTATCGAGGGAGAAGTGAAGGACTCCATTGCAGGGGGCGTGTGGTTCAAGTCCCAGATTAC
 TAAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAAGTCCCAGATTAC
 GATGAGGAGGCCACCTGGGAGCTGCAGGACTGGCTCACTCCCTCTCATTCCAT
 CGTGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTCCCCCAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTCTTCAGACTCCAGAGCAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTGCTGAGCAGACTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTCCAGCCCTCACCTGGCCTGGCTTCTATTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTATGGGAGTATAATTGTTCTCAAATCCAAGGGAAAATCCA
 GGCAGAACCTGGACTGGAGAAGAACGACGGACAGGCAATTGAGAGACGCCGGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCGAAGCTCTGCCTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGAGTGTCGGGATGACGTAGACAGGGGAAAGAACAAATGTG
 ACTTTGTCTCCAAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTCAC
 ATTCAATCCCCATTATCAGCCTCCCCCCCAGCACCCCTCTACACGAGTAGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTCAATAACAAATGACCAGTCCCTATTATACC
 CTGCTGACATGTCAGTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTATGACGA
 GGAAAAGGGGACTCCCATATTCAATGTCAGTGTCTGGGA**TGA**GACAGAGAACCCCTG
 CTAAAGGGCCCCCACACCACAGACCCAGACACAGCCAAGGGAGGTGCTCCGACAGGTGGC
 CCCAGCTTCTCTCCGGAGCTGCGCACAGAGAGTCACGCTTCAAGTGGGAGC
 TGAGGTTCTCTGCCCTGAGCCCTGCAGCAGCGGAGTCACAGCTTCAAGTGGGGAG
 TGGCCTGACCCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGAGCGGAATAGACTCA
 CATTAGGTTAGTTGTGAAAACCTCCATCCAGCTAAGCGATCTGAACAAAGTCACAACCTCC
 CAGGCTCCTCATTGCTAGTCACGGACAGTGATTCTGCCTCACAGGTGAAGAGATTAAAGAGA
 CAACGAATGTGAATCATGCTGCAGGTTGAGGGCACAGTGTGCTAATGATGTGTTTA
 TATTATACATTTCCCACCATAAACTCTGTTGCTTATTCACATTAATTACTTTCTCTA
 TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTGTGAGGCTCAAAGAATAAAGAG
 GAGGTAGGATTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG
 AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAAAA
 TTCTAAATAAAATTAAACAAATTAAACTAAACATATTTAAAGATGATATATAACTACT
 CAGTGTGGTTGTCCCACAAATGCAGAGTTGTTAATATTAAATATCAACCAAGTGTAAATT
 CAGCACATTAATAAAGTAAAAAGAAAACCATAAAAAAAAAAAAAAA

FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pi: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGILCGALC
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRKSVASQGFQAGRHYWEVDVGQNVGVYVGCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTCATTGCTGGTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTGTTGGAACCCCTGGGTTATCGGCCTCGTCATCTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTCATTATGTGAGATATAATCAAAGAACGACTACAA
 TTACTATAGCACATTGTCATTACAACGTACAAACTATATGCTGAGTTGGCAGAGAGGCTT
 CTAACAATTTACAGAAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTTATAAA
 TCTCCATTAAGGGAGAATTGTCAAGTCTCAGGTTATCAAGTTCAAGTCAACAGAACGATGG
 AGTGTGGCTCATATGCTGTTGATTTGAGATTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAATTGTTCAACTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCTAAAGTA
 GATCCTCACTCAGTAAAATAAAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCA
 TTGCTCGGAACACGAAGAAGTAAAACCTCTAGGTAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGCCCTGGCAGGCTAGCCTGCAGTGGATGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGAGTGCTGCTCACTGTTACAACATATAA
 GAACCTGCCAGATGGACTGCTTCCTTGGAGTAACAATAAAACCTCGAAAATGAAACGGG
 GTCTCCGGAGATAATTGTCCATGAAAATACAAACACCCATCACATGACTATGATATTCT
 CTTGCAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTCTCCCTGA
 TGCAATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTTGGAGCACTGAAA
 ATGATGGTTACAGTCAAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACA
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGAECTCTGGAGGACACTGGTTAGTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCAACAAG
 CCTGGTGTATAGAGTTACGGCCTGCGGGACTGGATTACTTCAAAACTGGTATC**TA**
AGAGACAAAAGCCTCATGGAACAGATAACATTGTTGGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAAC
 TGTTGCTTGATGCATGTATTTCTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCTAGAAGTTGTGAGAATTTCAGAATTTGAC
 TTGTTGACATAAATTGTAATGCATATACAAATTGAAAGCACTCCTTCTCAGTTCTC
 AGCTCCTCTCATTTCAGCAAATATCCATTGCAAGGTGAGAACACAAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAAATCCCCTACATTGAGAACAGAAAAGTATTAGGTGTTCTTAGT
 GGAATATTAGAAATGATCATATTCACTATGAAAGGTCAAGCAAAGACAGCAGAACATCA
 ACTTCATCATTAGGAAGTATGGAACTAAGTTAAGGAAGTCCAGAACAGCAAGATATA
 TCCTTATTTCTTCAAAACAACTACTATGATAAATGTGAAGAACAGATTCTGTTTTGTG
 ACCTATAATAATTACAAACTCATGCAATGTACTTGTCTAAGCAAATTAAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAACACCCCA

FIGURE 150

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAYKSPREEFVKSQVIKFQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCTRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATLVSAAHCFETYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPHDYDISLAELOSSPVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTCCAGCAAACGGCATTGAAGTTGAAGATAAACCTGACAGCA
 CAGCCTGAGATCTGGGATCCCTCAGCCTAACACCCACAGACGTAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGCTCTCCCTGCCTTGTGGCTCCTGGC
 CGTGACCTCTGGTCCCAGAGCTAGCCCTGGCCCTCAAGACTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCCCTTGCCGGCTGTCCCCCTGCGACTACGACCACTGC
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCCTGCCTGTGCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCATGGAGAAGTGCCTGCATTGC
 CCGAAGAGGGCCGCCAGTGGTCCACTGGTGTGCCCTCTCCCCGGCTCCACTACTGG
 CTGCTGCTTGGGACGGCAGCGAGGCTGCGCAGAAGGGCCCCCGCTGAACGCTACGGTCC
 CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGCAATTATGTCGTTGCGTAGTGGCCGCTA
 ACGAGGCCGGGCAAGCCGCGTGCCTCAGGCTGGAGGAGAGGGCCTCGAGGGGCCGACATC
 CCTGCCTTCGGGCCTTGCAGCCGCCCTGCGGTGCCGCCAACCCCCGCACTCTGGTCCACGC
 GCCGTCGGGTGGCACGCCCTGCCCTGCTAACGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCATCGCTGGGCTGCCGCCGAGCCGCCGAGCCGCAGGGCGCT**TGA**
 AAGGGGCCTGGGGCATCTGGGCACAGACAGCCCCACCTGGGCGCTCAGCCTGCCCG
 GGAAAGAGGAAAACCGCTGCCCTCAGGGAGGGCTGGACGGCGAGCTGGAGGCCAGCCCCAG
 GCTCCAGGCCACGGCGAGTCATGGTCTCAGGACTGAGCGCTTGTAGGTCCGGTACTT
 GCGCTTGTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGCCCCAATTTTTTA
 AGCGGCCAGATAATAATGTAACCTTGCGGTTAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPPLNATVRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVHAAVGVGTALALLSCAALVWHFCLRDRWGCPRAAARAAGAL
```

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCCGAAGAAGTTCC
 CTGCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCAGGCAGGCGTGGGCACCGGG
 CCCAGCGCCGACGATCGCTGCCGTTGCCCTGGGAGTAGGATGTGGTGAAAGGATGGGGC
 TTCTCCCTTACGGGCTCACAA**TG**CCAGAGAAGATTCCGTGAAGTGTCTGCCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTTGGTTAATGTCCATCAGTGTGGCAGTTCTGCTTGG
 TGAGGGACTACCTAATAATGTTCTCACTTAAC TGCAAGAACGAGGGTAGAGGAAGCAGTC
 ATTTGACTTACTTCCCTGTGGTTCATCCGGTCA TGATTGCTGTTGCTGTTCCATTATCAT
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTGCATGGTACT
 TTGGAAAGTTGCTTGTCA TTTCTGTGTTAGAACTGGCTGTGGCGTTGGACATATGAACAG
 GAACTTATGGTCCAGTACAATGGTCAGATATGGTCAC TTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTCAGAGAGAGTTAAGT
 GCTGTGGAGTAGTATATTCACTGACTGGTGGAAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTTAGAGAATTCC CAGGATGTTCAAACAGGCCACCAGGAAGATCTCAGTGA
 CCTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCTTTGAGAGGAACCAAACACTGC
 AGGTGCTGAGGTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGCTCTGTATTATGATAGAAGGGAGCCTGGACAGACCAAATGATGTC
 CTTGAAGAATGACA ACTCTCAGCACCTGTCA TGCCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTAAATACACACTTGAGATGGAG
 GAGTTA**TAAA**AGAAATGTCACAGAAGAAAACCACAAACTTGTTTATTGGACTTGTGAATT
 TTTGAGTACATACTATGTGTTCA GAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTAAATGAGGATGGAAAAGTTCATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTACTGAACACAGTTATGTTGAGGCAGCATGGTTGATTAGCATTTC
 CGCATCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGTTGATTTACTT
 CTACCAACTAGTATATAAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTATTACTCAGCGATCTATTCTGATGCTAAATAATTATATCAGAAAATTT
 AATATTGGTGA CACTACCTAAATGTGATTTGCTGGTTACTAAAATATTCTACCACTAAAA
 GAGCAAGCTAACACATTGCTTAAGCTGATCAGGGATT TTGTATATAAGTCTGTGTTAAA
 TCTGTATAATTCA GTGATTCTAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
 ATTTGTCTGTATAGCATCATTATTAGCCTTCTGTTAATAAAAGCTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTAAATACTTAACCACTAATTGAAAATTA
 CCAGTGTGATACATAGGAATCATTATTCA GAAATGTAGTCTGGTCTT TAGGAAGTATTAATAA
 GAAAATTGCACATAACTTAGTTGATTCA GAAAGGACTGTATGCTGTTCTCCAAATG
 AAGACTCTTTGACACTAACACTTTAAAAGCTTATCTTGCCCTCTCCAAACAAAGAA
 GCAATAGTCTCCAAGTCAATATAAAATTCTACAGAAAATAGTGTCTTTCTCCAGAAAAT
 GCTTGTGAGAATCATTAAAACATGTGACAATTAGAGATTCTGTTATTCACTGATTA
 ATATACTGTGGCAAATTACACAGATTATTAATTTTACAAGAGTATAGTATATT
 GAAATGGGAAAAGTGCATTTACTGTATTTGTGTTATTCTCAGAATATGGAA
 AGAAAATTAAAATGTGTCATAAAATATTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLNLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMWDPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFGLGISIGVTQILAMILTITLLWAL
YYDRREP GTDQMMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTGCTCAGCGAACAGGATGCTGGCGTGAGGGACCAAGGCCTGCC
 TGCACCTGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTGGGGTACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGAAACCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGAACTGGTCTGCGCTGTTGACAACCTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTCGATCGGAACACTCAAGTGGCCCTGTC
 TCTCAGGCTCCCTGGCTCCCTGCACTGTCTGCCTGTGGGAAGAGCCTGAAGACCCCCCGT
 GTGGTGGGTGGGGAGGAGGCCTCTGGATTCTTGGCCTTGGCAGGTCAAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATTGGACCCCCACTGGTCCTCACGGCAGCCCAC
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCATGTACCCAA
 AGACAATGACATGCCCTCATGAAGCTGCAGTCCCACACTCACTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGA
 TGGGGCTTACGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCAATTGACAGCACCGTGCAATGCAGACGATGCGTACCGAGGGAAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGAAGGGGTGTGGACACCTGCCAGGGTACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGCATCGTTAGCTGGGCTATGGCTGCGG
 GGGCCCAGCACCCAGGAGTACACCAAGGTCTCAGGCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTGCACTGCTGGAGCCGCTCCTCCTG
 CCCTGCCACCTGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCCTGGTACACCC
 CTCTGCCACAGCCTCAGCATTGAGCAGCAAAGGGCTCAATTCTGTAAGAGACCC
 TCGCAGCCCAGAGGCAGAGGAAGTCAGCAGCCTAGCTGCCACACTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCACCTGAACAAGGTCTCAGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGAAAAGCCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGTCCGTCTCACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCACTGTGGTATGACTACCGTT
 ACCTACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAA

FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVVLIKVILDKYYF
LCGQPLHFI PRKQLCDGEELDCPLGEDEEHCVKSFP EGP AVAVRLSKDRSTLQV LDSATGNWF
SACFDNFTEAL AETACRQM GYSRAVEIGPDQ DLDV V EITEN SQEL RMRN SSGP CLSGS LVSL
HCLACGKSLKT P RVVG GEEAS VD SWP QV SIQ YDK QHV CGGS IL DPHW VL TAAHC FRK HTDV
FNWKVRAGSDKLGSFPSLAVAKIIIIFNPMPKDNDIALMKLQFPLTFSGT VRPI CLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDT CQGD SGGL MYQSDQWHVVGIVSWGYGC GG P STPGV YT KVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGCATCCCCAGGCTCCAG
 AGCTCCCTGGTGACAGTCTGTGGCTGAGC**ATG**GCCCTCCAGCCCTGGCCTGGACCCCTGGAGCCTCTGGCC
 TTTCCCTTCCAAGTCTGCTCAGCTGCTGCCAGCAGCAGCGGGGGAGGCAGGGCAGGGCCATGCCA
 GGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAAGGGCCTCCAGGATTTGACA
 CTCTGCTCTGAGTGGTATGGAAATACTCTACGTGGGGCTCGAGAACGCATTCTGGCCTGGATATCCAGG
 ATCCAGGGTCCCCAGGCTAAAGAACATGATAACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTA
 AGAAGAACAGCAATGAGACACAGTGTTCACACTCATCCGTGCTGGTTCTTACAATGTCACCCATCTAC
 CCTGCGGCACCTCGCCTCAGCCCTGCTGTACCTCATTGAACITCAAGATTCCTACCTGTTGCCATCTCGG
 AGGACAAGGTATGGAGGGAAAGGCCAAAGCCCCTTGACCCGCTCACAGCATAACGGCTGCTTGGTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACTCCTGGCAGTGAGCCATCCTGATGCGCACACTGGGATCCCAGC
 CTGTCCTCAAGACCGACAACCCCTCGCTGCATCATGACGCTCCTTGTGGCAGCCATCCCTCGACCC
 AGGTGCTACTTCTTCGAGGAGACAGCCAGCGAGTTGACTTCTTGAGAGGGCTCACACATCGGGTGG
 CTAGAGTCTGCAAGAACATGACGTGGCGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTCTGAAGGCCAGC
 TGCTCTGCACCCAGCCGGGGCAGTGCCTCAACGTATCCGCCACGCCGCTGCTCCCCGCCGATTCTCCA
 CAGCTCCCCACATCTACGCAGTCTCACCTCCAGTGGCAGGTTGGCGGGACCAGGAGCTGCGGTTGTGCCT
 TCTCTCTTGGACATTGAACGTGTTAAGGGAAATACAAAGAGTGAACAAAGAAACTTCACGCTGGACTA
 CTTATAGGGCCCTGAGACCAACCCCGCCAGGCAGTTGCTCAGTGGCCCTCTGATAAGGCCCTGACCT
 TCATGAAGGACCATTCCTGATGGATGAGCAAGTGGTGGGACGCCACTTGTGATGTACCTGGGAACCAACACAG
 GGTGCTCCACAAGGCTGTTAAGTGGGACAGCAGTGCTCATCTGGTGAAGAGATTGAGCTGTTCCCTGACC
 CTGAACCTGTCACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTGAGGCTCTCAGGAGGTGTCTGGA
 GGGTGGCCCGAGCCAAGTGTAGTGTCTATGAGAGCTGTGACTGTGCTTGCCTGGGGACCCCACTGTGCCT
 GGGACCCCTGAGTCCGAACTGTTGCCCTCTGCTGCCCTGGGGACCCCAACTGAACTCCTGGAAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGCATGTGCCAGTGGCCCTGAGCAGGAGCCTCGGCCCTAGAGCCGCCGCAAATCATT
 AAGAAGTCCTGGCTGCCCCAACTCCATCCTGGAGCTCCCTGCCCTGAGCAGGCTTGTGCTGAGCTGGCTTATTATT
 GGAGTCATGGCCAGCAGCAGTCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTTGTGATAGTGCAGG
 ATGGAGTTGGGGTCTTACCAAGTGTGGCAACTGAGAATGGCTTTCATACCCGTGATCTCCTACTGGTGG
 ACAGCCAGGACCAACCTGGCCTGGATCCTGAACGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA
 CCAGGGTCAGTGGTGGGCCCTGGCTGCCAGCAGTCTACTGGCCCTACTTGTCACTGTCAGTGCCT
 TTGCTTAGTGCTTCAAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCAGTCCGGCTCGGGCAAGG
 TTCAGGGCTGTGAGACCCCTGCCAGTGTGGACGCTGACAACAACTGCCTAGGCAGTGGTAGCT**TAA**ACTCTAGGCA
 CAGGCCGGGGCTGGGTGCAGGCACCTGCCATGCTGGCTGGCGGCCAAGCACAGCCCTGACTAGGATGACAG
 CAGCACAAAAGACCACCTTCTCCCTGAGAGGAGCTCTGCTACTGCACTGATGACACTCAGCAGGGTG
 ATGCACAGCAGTCTGCCTCCCTATGGACTCCCTCTACCAAGCACATGAGCTCTAACAGGGTGGGGCTAC
 CCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTCAGTCTGGCCATTCCAGGGACCC
 CAGAAACACAGTGTTCAGAGACCCCTAAAAAACCTGCCCTGTCCCAGGACCCATGGTAATGAACACCAAAACATC
 TAAACAATCATATGCTAACATGCCACTCTGGAAACTCCACTCTGAAGCTGCCCTTGGACACCAACACTCC
 TCTCCCTAGGGTCATGCAGGGATCTGCTCCCTCTGCTTCCCTACCAAGTGTGACCGCTGACTCCCAGGAAGTC
 TTTCCCTGAAGTCTGACCACCTTCTTCTGCTCAGTTGGGGCAGACTCTGATCCCTCTGCCCTGGCAGAATGG
 CAGGGTAATCTGAGCCTCTTACCCTAGCTGACCCCTCACCTCTCCCCCTCCCTTTCTTGT
 TTTGGGATTCAAGAAAATGCTTGTAGAGACTGTTATTTTATTAAAAATATAAGGCTTAAAAAA

FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLLQLLLPTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHDASFVAIIPSTQVVYFFF
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPIYAVFTSQWQVGGTRSSAVCAFSIILDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFIMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTOGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYYSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTAGCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGGCTTCCGTAGAAG
 TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTAGTGGCTTCCTCCCTGGGTCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG
 GTCCTTTATGCCAGATTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTAAAAAGAGTTGATTCTGGAAAGAAACTTGTAGG
 TGGCAGAGGAAAATTGAAAACCTATTAAATGTTCTAGAATACTTGGCCTGCAGTGCAGTC
 ATTTTTAAATAGAAAGGATATCATGGATTCTAAAGAATGAGAACATTCGACATGGTGATA
 GTTGAACACTTTGACTACTGTCCTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
 CATTCTTCACTTCATTGGCTCTTGGATTGGCTACCAATCCCCCTGTCTATGTT
 CAGTATTCCGTTCTGACTGATCACATGGACTCTGGGGCCGAGTGAAGAATTCTG
 ATGTTCTTAGTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
 GGAACATTTACAGAAGGCTTAGGCCAGTTGTCTCATCTTCACTGAAAGCAGAGTTGT
 GGTCATTAACACTGACTTGCCTTGATTGCTCGACCTCTGCTCCAAACACTGTTAT
 GTTGGAGGCTTGATGGAAAACCTATTAAACCAGTACCAAGACTGGAGAACATTGTC
 CAAGTTGGGACTCTGGTTGTGACCTTGGCTCATGGTAACACCTGTCAGA
 ATCCGAAATCTCAAGGAGATGAACAAATGCCCTGTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCACTGTTCTCATTGCCAAAGATGTCACCTGGCTGCAAATGTGAAAATTGTT
 CTGGCTCCTCAGAGTGACCTGGCTCACCAAGCATTGGCTGTTGTCACCCACGGCG
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGATCCCTCT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAACGCAAAAGTTGGTGTTCATTGAGT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGAAAGACAAGAGAT
 ACAAGTCCGGCAGTGGCTGCCAGTGTCACTCTGCGCTCCCACCCGCTCAGCCCCACACAG
 CGGCTGGTGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCAGCACCTCAAGCCCTA
 TGTCTTCAGCAGCCTGGCATGAGCAGTACCTGTCACGTTTGTGTTCTGCTGGGGC
 TCACTCTGGGACTCTATGGCTTGTTGGAGCTGCTGGCATGGCTGTCTGGTGGCTGCGT
 GGGCCAGAAAGGTGAAGGAGACA**TAA**GGCCAGGTGCAGCCTGGCGGGCTGTGGTGG
 GCGATGTCACCATTCTAGGGAGCTTCCACTAGTTCTGGCAGCCCCATTCTAGTCCTTC
 TAGTTATCTCCTGTTCTGAAGAACAGGAAAATGCCAAAATCATCCTTCACTTGC
 TAATTTGCTACAAATTACATCCTTACTAGCTCTGCTGCTAGCAGAAATCTTCACTGCT
 CTTGTCCTCTTGTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTGAGTGACTTG
 GACCACTGACCCCTCAGATTCCAGCCTAAACATCCCTCTCATGCGCTCTCCGAA
 TCACACCCCTGACTCTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCACTCCTGCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTGCATATTCTTCAGTTCTGTT
 TGTTCTCCCACATATTCTCTCAATGCTCAGGAAGCCTGCCCTGCTCTGGTCCCCACAGT
 CGGACACAGGCTCACAGGTCTCCACATTGGCTCCATGGTCCCCACAGTGA
 GCTTGGCTGAGCAGGCATGGAGACTGTAGGTTCCAGATTCTGAGAATTTA
 GCGTTATCTCCCCAACCTCACTAA

FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLVGFLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTMLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIDMSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF
INSDFAFDFARPLLPTVYVGGLMEKPIKPVQPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPPLFGDQOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPPLSPTQRILVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDVFVFLGLT
LGTLWLCGKLLGMAVWWLRGARKVKET
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGATTTGAAGAGAGGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTCACACCGTCACACACATACCATGTT
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCCTCCCACCCAGCAGGGCTACCCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGGCTTCATCCCTCCTCTCCAAAGCCCA
 ACTGCTGTCAGTGCATGCTCTGCCAAGGAGGAGGAACTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGTTCAGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCAGGGTGGAGAATCCAGGGAGGAGGAGCGAAAACAGAACAGAGGGCAGA
 AGACCGGGGCACTGTGGGTTGCAGAGCCCTCAGCC**ATG**TGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCCTACACAGTCCCAGGCTGCCCTGGTTCTGGTGCCTCTGCCCTGGGGC
 GGGTGGGCCAGGAGGGTCAAGAGCCCTGCTGGAGGGGAGTGCCTGGTGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTGCTGCGGTCCGAAGCCACCACATGAGCCAGCAGGGAAACCGGCAATGGC
 ACCAGTGGGCCATCTACTTCGACCAAGGTCTGGTGAACGAGGGCGGTGGCTTGACCGGGC
 CTCTGGCTCCTCGTAGCCCTGTCCGGGTGCTACAGCTCCGGTCCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTATCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTGTGCTACTGCCCTGGA
 CCCTGGGACCGAGTGTCTGCGCCTGCGTCGGGGAATCTACTGGGTGGTGGAAATACT
 CAAGTTCTGGCTCCTCATCTTCCCTCTC**TGA**GGACCCAAGTCTTCAGCACAAGAAT
 CCAGCCCTGACAACCTTCTGCCCCCTCTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCCACCTTTGCATGGACCCCTGTGCCAAACACCCAAAGTTAA
 GAGAAGAGTAGAGCTGGCATCTCCAGACCAGGCCTTCCACCCACCCACCCAGTTAC
 CTCCCAGCCACCTGCTGCATCTGTTCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA
 AGAAGGAAGATCTGACTACTTGCGGCCTGCTCCTCCGGTCCCCACCCAGCTTCC
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCCAG
 ATGGACAAGCCTCAGCGTACCCCTGCAGGCTTCTCCTGTGAGGAAAGCCAGCATCAGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGCTAGGGTGGGAGGCTAGCCAC
 AGGCAGAAGGGTGGGAAGGGCTGGAGTCTGGCTGGTGAGGAAGGAAGGAGGGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCCTCTATGCTGGATCCCAGATGGACTCTGCCCTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCAGTCATCCTCTGCTGGCCACCTCCTGAAACTGCTCCAC
 CTTGAGTTGAACCTTAGCCCTCCACACTCTGACTGCTGCCCTCCTCCCAGCTCTC
 TCACTGAGTTATCTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCCTGAT
 CTGTGCTGCTTATTCTCCTCCCTAGGCTTCTATTACACTGGGATTCCATGATTCAATTCTT
 CAGACCCTCTCCCTGCCAGTATGCTAAACCCCTCTCTTCTTCTTATCCGCTGCTCCATT
 GGCCCAGCCTGGATGAATCTATCAATAAAACAATAGAGAATGGTGGTCAGTGAGACACTAT
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTGGATGGGTGTTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAATAATCAAACGTATACTAAAATTAAAAA

FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVILLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSLMLNTWPVISAFAANDPDVTREAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

Signal peptide:

amino acids 1-32

FIGURE 163

GCTGTTCTCGGCCACCACTGGCCGCCGGCGCAGCTCCAGGTGTCCTAGCCGCCAGC
 CTCGACGCCGTCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGCGGGGCAT
 GGGCCAGGGCGCGGGTGAAGCGGCTCCCGGGGCGTGACTGGCGGGCTTCAGCC**AT**
GAAGACCCTCATAGCCGCCTACTCCGGGTCTCGCGGGCAGCGTCAGGCCGAGGCTGACC
 GGAGCCAGCGCTCTACGGAGGACCTGCGCTGCGCGAGGGCTGGGAGATGGGGCACT
 GGATCCAGCATTCTCCGCCCTCCAGGACCTTCTGTACCTGGCTCAATAGGTCAA
 GGTGGAAAAGCAGCTACAGGTATCTCAGTGCTCCAGTGGCTCTGTCCTCCTGTACTGG
 GAGTGGCCTGCAGTGCATGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTCATCGCTGTG
 CTCTACTTCACTGGCTGGTGTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTACA
 GTGGGTCCGAAACTGGCTGTGGCCTACTTCGAGACTACTTCCCATCCAGCTGGTGA
 AGACACACAACCTGCTGACCACCAGGAACATATCTTGGATACCACCCCCATGGTATCATG
 GCCCTGGTGCCTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTCCCAGG
 CATA CGGCCTTACCTGGCTACACTGGCAGGCAACTCCGAATGCCGTGTTGAGGGAGTACC
 TGATGTCTGGAGGTATCTGCCCTGTCAGCCGGACACCATA GACTATTGCTTCAAAGAAT
 GGGAGTGGCAATGCTATCATCGTGGTCGGGGTGCGGCTGAGTCTTGAGCTCCATGCC
 TGGCAAGAATGCAGTCACCCCTGCGGAACCGCAAGGGCTTGTGAAACTGCCCTGCGTCATG
 GAGCTGACCTGGTCCCCTACTCCTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTC
 GAGGAGGGCCTGGGGCGATGGTCCAGAAGAAGTCCAGAAATACATTGGTTGCC
 ATGCATCTCCATGGTCGAGGCCTTCTCCTCCGACACCTGGGGCTGGTGCCTACTCCA
 AGCCCATCACCACCTGTTGGAGAGGCCATCACCATCCCCAAGCTGGAGCACCAACCCAG
 CAAGACATCGACCTGTACCAACCCATGTACATGGAGGCCCTGGTAAGCTCTCGACAAGCA
 CAAGACCAAGTCGGCCTCCGGAGACTGAGGTCTGGAGGTGAAC**TGA**GCCAGCCTCGGG
 GCCAATTCCCTGGAGGAACCAGCTGCAAATCACTTTTGCTCTGTAAATTGGAAGTGTCA
 TGGGTGTCTGTGGTTATTAAAAGAAATTATAACAATTGCTAAACCAAAAAAAA
 AAAAAAAA
 AAAAAAAA

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVDWNTPKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMGGICPVSRTIDYLLSKNGSGNAIIVVGAAESLSSM
PGKNAVTLRNRKGFKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:

Transmembrane domain:

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGGGGGATGGGGCCGGGGCGGGCGGCACTCGCTGAGGCCCGACGCAGGCCGGCCGGCCA
 GGGCGAGGAGCGCGCGGCCAGAGCGGGCCGGAGGCAGCAGCCGGACGCCGCGACGAGCAGGTGGCG
 CGGGCTGCAGGCTTGTCCAGCGGAAGCCCTGAGGCAGCTGTTCCACTGGCTCTGCTGACCTTGCGCTTGG
 CGGCTGCCTCAGCGAGGGGCCGTGCACCCGCTCTGAGCAGCGCCATGGGCCTGCTGGCCTTCCTGAAGACCCA
 GTTCGTGCTGCACCTGCTGGTGGCTTGTCTCGTGGTAGTGGCTGGCATCAACTCGTCCAGCTGTGCAC
 GCTGGCGCTGGCCGGTCAGCAAGCAGCTCACCGCCCTCAACTGCCGCCTGCCTACTCACTCTGGAGCCA
 ACTGGTCATGCTGGTAGTGGCTGCACGGAGTGTACACTGTTCACGGACCAGGCCACGGTAGAGCGCTT
 TGGGAAGGAGCACGCAGTCATCATCCTCAACCACAACCTCGAGATCGACTTCCCTGTGGTAGGACATGTGTGA
 GCGCTCGGAGTGCTGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC
 GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG
 GCGCCTGCGACTACCCGAGTACATGTGGTTCTCCTGACTCGAGGGACCGCGCTCACGGAGACCAAGCA
 CCGCGTTAGCATGGAGGTGGCGCTGCTAAGGGGCTTCCTGCTCAAGTACCAACCTGCTGCCGCGGACCAAGGG
 CTTCACCAACCGCAGTCAGTGCCTCCGGGGACAGTCGAGCTGTATGATGTAACCTGAACCTCAGAGGAAA
 CAAGAACCGTCCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGGGACATGTGCGTAGGGAGATTCTCT
 GGAAGACATCCCCTGGATGAAAAGGAAGCAGCTCAGTGGCTCATAAACTGTACCAAGGAGAAGGACGCGCTCCA
 GGAGATATATAATCAGAACGGCATGTTCCAGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCTGAA
 CTTCTGCTGGGCCACCATTCTCTGCTCCCTCTTCAGTTGTCTGGCGTCTTGCCAGGGATCACC
 TCTCCTGATCCTGACTTCTTGGGTTGTGGAGCAGCTCCTTGGAGTCCGAGACTGATAGGAGAATCGCT
 TGAAACCTGGGAGGTGGAGATTGCAGTGAGCTGAGATGGCATCACTGACTCCAGCCTAGGAACAGAGCAAGACT
 CAGTCTAAAAAAAAAAAAACAAAAACCCAGAAATTCTGGAGTTGAACGTGTTACTGACATGAAAA
 ATTCACTAGAGGCTAACAGCAGATTGAGCAGGGAGAAAAATCAGCAAGCTGAAGATGGTACCTGAGATT
 TTTCAGGCTAATGAAAAAGAATGAAGGAAATTAAACACCCCTCAGAGACCCATGGTCACCGTCACACAAATCAA
 CATATGCATGATGAGAGTCCCAGAACGGAGAGAAAGGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA
 GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTCAT
 AATCAAAGTCAATGACAAAGAATCTGAAAGCAGCAAGAGATGAGCAACTTATCTGTTCAAAGGATCTTG
 ATCAGATTAACAGCTCATTCTCCTCAGAAATCATGGGAGCCAGGGAGATGAGCTGAAACACTGTTGAAGGCAA
 AACCTCAACTGTAATTATTGGACTTTGAGCTTAGATGGCCTGACCTCTTGCTTCAGGGACAGTTTCA
 ATTTAATCCCTAATAACAATTAGTCAGCTTGTGACCTGTAGGAAGGCTGTCTTAGGCCGGCACAGTGGC
 TTACACCTGTAATCCCAGCACTTGGGAGGCCAGACGGTGGATCATTTGGGTCAGGCTGATCTCAAACCTCCT
 GAGTTAGGTGATCTGCCGCTCAGCCTCCAAAGTGTGATTGCAGGCGTAGGCCACTGCGCTGGCCGG
 ATTTCTTTAAAGGCTGAATGATGGGGCCAGGCACGATGGCTCACGCCGTGATCCAAAGTAGCTGGATTGTA
 AACATGCACCACCATGCCCTGGCTAATTGTATTAGTAGAGACGTGTTAGCCAGGCTGGCTCGATCTCCT
 GACCTCAAGTGACCACCTGCCCTGCCCTCCAAAGTACTGGGATTACAGGCGTAGGCCACTGCGCTGGCCTTGA
 GCATCTTGTGATGTGCTTATTGCCATTGTATATCTTCTATCTTCTTGGGAAATGTCTGTTCAAGTCCTT
 CCTTTTAAATTATTATTATTATTATTGAGACAGGGCTTGTGTTCTGGCCAGGCTGGAGTA
 CAGTGGCACAGTCTGGCTCACTGCAGCCTGCCACCTCCTGGCTGAGTGTACTCTCCACCTCAGCCTCCCT
 AGCTGTATTGTATTGTATTGTAGCTGTTAGCTGTTGTATTGTGGAGACAGCATTCAACCATGA
 TGCCCAGGCTGGCTTGAACCTCTGAGCTCAAGTGTACTGCTGCCCTCAGCCTCCAAAGTGTGGGATTACAGA
 CATGAGCCACTGCACCTGGCAAACCTCCAAATTCAACACACACACACACACACACACACACACACACAC
 GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTGGCATGAGAAGTCGAGGCTG
 CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAAACAGAGTGAGACCCGTCTC

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVSGLVINFVQLCTLALWPVSKOLYRRLNCRAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFIEDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPDKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSTVLGVFASGSPLLILTFLGFVGAASFGVRRILIGESLEPGRWRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTATTTAAGAACCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCTGGGCA
 GCCACCAGGCATATTCATCTTGTGTGTTTCTTGCTTAGCACTGGGCACCTCTT
 GCTTATTTCTTGGTAGGAAAGGGCAGTTGTCTGGGTTGGTGGCAGGCAGGCCG
 GCTTACGCCTGATAACGCCCTGGGTTAGAAGGAAGGAAGATAAACTTTATACAAATGGG
 GATAGCTGGGTCTGAGACCTGCTCCTCAGTAAAATTCTGGATCTGCCTATACCTCTT
 TTCTCTAACCTGGCATACCCTGCTAAAGCCTCTCAGGGCTCTCTGTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTCATTGT
 ACATGTGGTGTCTTGTCGTTCTG**TAA**TGTGGTATGCCATGGGTCTTGACAAAGCCT
 TTCCTCTTGGCTGGACACTGTTCCCTGCCCCCCCCACTCTTCTACTTAATATGTAGTC
 ATCCTGCAGATTCAATTCTAACATCATTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTTGTTAATGCTCTCATAACGACACTGTTCCCTTGCAGCACTGCCACTCAGTGTA
 TCTTATGTGCGTTGTGGTTGTATGGTTGTCTGTTCCCCAGAATGCCAGCTTGAGC
 TGCAGGGTCAAGGCATTGCTGTGCCTGCCAGGTATAGTCCTACATGTGGTGGTGCT
 CATGTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTCACCA
 GATGGTGTAGGGCCCAGCATTGAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGA
 TGCAGGTCTGATTCACTAGGCCAGGTTGGCATCTCTAACAAACTCCCACGTGATGCTGA
 TGCTGGCCTATGAACCTAAATAGTAAGAACATGGAGCCAGGCTGGCATGGTGCT
 TCACACCTATGATCCCAGCACTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGCCAACATGGGAAACCCATCTGACTAAAAAACACAAATTAGCTG
 GGCAATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAACGCTTG
 AACCTGGGAGGCGGAGGTTGAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAAA

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSIQCPCGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSGVGGRQAGLRLIRPWVRR
EGKINFYTNNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPEPSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCAAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAAC TGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTAAAATCTGTTTTGTTCTTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCAAACCTGACCTCACCTGACTCTGGAACGAGAACAGAGGTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCACGTCTGGAGGACTGACTCGGGCAGTCAGGTAGCTGAGCCTCTGGTA
 GCTGCGGCTTCAAGGTGGCCTTGCCTGGCGTAGAAGGGAT**TGA**CAAGCCGAAGATT
 CATAGGCGATGGCTCCACTGCCAGGCATCAGCCTGCTGTAGTCATCACTGCCCTGGGG
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCGCCAT
 CTAACCTTTCATGTCCTGCACATCACCTGATCCATGGCTAATCTGAACCTGTCCCCAAGG
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGGAAAGGAACCTGTGCCAAATTATGGGTCAAGAAAGATGGAGGTGTTGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGAAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGATCCACGTACCAAGCTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAATCTGCGATCACCAG
 CCAGGGCAGCGTCTGGAAAGGAGCAAGCAAAGTGACCATTCCTCCCTCTCCCTC
 TGAGAGGCCCTCCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGCTAATG
 GCTCAGTGTGGCCAGGAGGTCAAGCAAGGCCTGAGAGCTGATCAGAAGGGCTGCTGTGCG
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGAAAATCCCCAGGCAAAGGACTGTGTGGCT
 CAATTAAATCATGTTCTAGTAATTGGAGCTGCCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGCCCTTATAACCCAGGAGACTTGTATTGCGGGTGTGGTGGCTGTAATG
 CCAACATTTGGAGGCCGAGGCAGGCTAGATCACCTGAGGTCAAGGAGTTCAAGACCAGCCTG
 GCCAACATGGTGAACCCCTGCTCTACTAAAAATACAAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAAACCTGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAGAATTATGGTTATTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRD
```

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCTCCTGCCCGGCC**ATG**ACCCAGCCGGTCCCCGGCTCTCCGTGCCCGCGCT
GGCCCTGGGCTCAGCCGACTGGCGCCGCCTCGCCACTGGCCTCTTCCCTGGGGAGGCGGT
GCCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGAACAGCCGCCTGTGG
CAGTATCTCTGAGCCGCTCCATGCAGGGAGCACCCGGCGCTGCGAACGCTGAGGCTGCTGAC
CCTGGAGCAGCCGCAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTTGGCCAACC
TGGCGGGCTCATCCAGGCCAAGAAGGCCTGGACCTGGCACCTCACGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCGGGACGGCGCGTGGTACCTGCGAGGTGGACGCGCA
GCCCGGAGCTGGACGGCCCTGTGGAGGCAGGCCGAGGCAGCACAAAGATCGACCTCC
GGCTGAAGCCCCTGGAGACCCCTGGACGAGCTGCTGGCGCGGGCGAGGCCGGCACCTTC
GACGTGGCCGTGGTGGATGCGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGCTGCGACCCGGAGGCATCCTGCCGTCCAGAGTCCTGTGGCGCGGAAGGTGCTGC
AACCTCCGAAAGGGACGTGGCGCCGAGTGTGCGAAACCTAAACGAACGCATCCGGCGG
GACGTCAGGGTCTACATCAGCCTCCTGGCGATGGACTCACCTGGCCTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGCTCGAGGGAGGGTTGCCTGGAACCCAGGAATTGAC
CCTGAGTTAAATTGAAAATAAGTGGGCTGGACACAAAAAAA

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPWGRREQCLLPPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDSSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGCAGCCGCTACCGCCGTGCAGCCGCTTCCGGCGCTGGGCCTCTGCCGTCA
 GCATGCCACACGCCCTCAAGCCCAGGGACTTGGTGTTCGCTAACAGATGAAGGGCTACCCCTCAC
 TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCCACCAACAAGTACCC
 CATCTTTCTTGGCACACAGAAACAGCCTCTGGACCCAAGGACCTGTTCCCTACG
 ACAAAATGTAAAGACAAGTACGGGAAGGCCAACAAAGAGGAAAGGCTCAATGAAGGGCTGTGG
 GAGATCCAGAACAAACCCCCACGCCAGCTACAGCGCCCCCTCGCCAGTGAAGCTCCTCGACAG
 CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG
 GGGTCATGGCCGTACAGCGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA
 GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCCTGCCTAAAGATGTC
 GGTCTCGAAACGAGCCCAGAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAACGACCGAGCGACCAGGACTTCACACCT
 GAGAAGAAAGCAGCGGTCCGGCGCCACGGAGGGGCCCTCTGGGGGACGGAAAAAAAAGAA
 GGCAGCGTCAGCCTCGACTCCGACTCCAAGGCCGATTGGACGGGCCAAGCCTGAGCCGG
 TGGCCATGGCGCGGTGGCGTCCCTCCCTCCCTCCCTCCCTCCGACTCCGATGTG
 TCTGTGAAGAAGCCTCCGAGGGGCAGGAAGCCAGCGGAGAACGCTCTCCGAAGCCGCGAGG
 GCGGAAACCGAAGCCTGAACGCCCTCCGTCCAGCTCAGCAGTGACAGTGACAGCGACGAGG
 TGGACCGCATCAGTGAGTGGAAAGCGGGAGCAGGCGCGAGGCGCAGCTGGAGGCCCGG
 CGCGGGCGAGAGCAGGAGGAGGAGCTCGGGCGCTCGGGAGCAGGAGAACGGAGGAGAACG
 GCGGAGGCGCAGCGGGCCGACCGCGGGGAGGCTGAGCGGGGAGCGGGCGAGCAGCGGGG
 ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAACGGGAGCAGCAAGGCCGGCGGGGT
 CCCCCGTCCTCCTCTGACTCCGAGCCGAGGCCGAGCTGGAGAGAGGCCAAGAAATCAGC
 GAAGAACGCCAGTCCTCAAGCACAGAGCCGCCAGGAAACCTGCCAGAACGGAGAACGAG
 TGCGGCCGAGGAGAACACAAGCCAAGGCCGTGAAGGTGGAGCGGACCGGAAGCGTCC
 GAGGGCTTCGATGGACAGGAAGGTAGAGAACGAGAACGCCCTCCGTGGAGGAGAACG
 GCAGAACGCTGCACAGTGAGATCAAGTTGCCCTAAAGGTGACAGCCGGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGGAACCTGAGGTGACCTCTCAGATCCTCCAGAAC
 ACAGACGTGGTGGCACCTGAAGAACGATTGCCGTTACAAAGCGAACAGGACGTAATGGA
 GAAGGCAGCAGAACAGTCTATAACCGGCTCAAGTCGGGTCTCGGCCAACAGATCGAGGCG
 TGCAGAAAGTGAACAAAGGCTGGATGGAGAACGGAGAACGCCGAGGAGAACGCTGGCGGGAG
 GAGCTGGCCGGGGAGGAGGCCAGGAGAACGCCGAGGACAAGCCCAGCGACATCTC
 AGCCCCAGTGAATGGCAGGCCACATCACAGAACGGGGAGAGCGCAGAGGACAAGGAGCAC
 AGGAGGGTGGACTCGGAGGAGGGCCAAGGTGTGGCTCTGAAGACCTGCACGACAGC
 GTACGGGAGGGTCCGACCTGGACAGGCCTGGAGCGACCCGGCAGGAGCGCAGAGGGCAGC
 GGGGGACTCGGAGGCCCTGGACGAGGAGAGCTGAGCCGCCGGCAGCCAGGCCAGCCCC
 CCGAGCTCAGGCTGCCCTCTCCTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAACGTGGG
 GAACGCTGTGCTTTGTATTGTTCCCTGGTTTTTCTGCCTAATTCTGTGATT
 TCCAACCAACATGAAATGACTATAAACGGTTTTAATGA

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNNKYPPIFFFGTHETAFLGPKDLPYD
KCKDKYGKPNKRKGNEGLWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDAEDDEDRG
VMAVTAVTATAASDRMESDSDKSSDNSGLRKTPALKMSVSKRARKASSLDQASVSPSE
EENSESSSESEKTSDQDFTPEKKAAVRAPRRGPLGGRKKKAPSASDSKADSDGAKPEPV
AMARSASSSSSSSSSDDVSVKKPPRGRKPAEKPLPKPRGRKPAPPERPPSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEERRERADRGEAERGGGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKSAKKPQSSSTE PARKPGQKEKRV
RPEEKQQAKPVKVERTRKRSEGFSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNAALEELGTIQLQTSQILQKNTDVVATLKKIRRYKANKDVMEEKAEEVYTRLKSRLGPKIEAV
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESEAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDRPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

FIGURE 175

GTGGGTTCTGGATCTCACCTTACCAACTGCAGATCTGGGACTCATCAGCCTCAATAATTATTAATTAAATTA
 ACACCATTGAAAGAGAACATTGTTTCATC**A**TGAATGCTAATAAGATGAAAGACTAAAGCCAGAACCCAAGA
 TTTCACCTTTCTGCTTGATGATGCTAACGATGACCATGTTGTTCTTCCAGTCAGTCAGTCAGTCAGTCAG
 AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTCAAATAGCTGTATTCCCTTTGGGTTCATC
 AGAAGGACTGGATTTCAAACTCTCTTAGATGAGGAAAGAGGCAGGCTGCTTGGGAGCCAAGAACCCACAT
 CTTCTACTCAGTCTGGTGACTTAAACAAAATTAAAGAAGATTATTGGCCTGCTGCAAAGGAACGGGTGGA
 ATTATGTAATTAGCTGGAAAGATGCCAATACAGAATGTGCAAATTTCATCAGAGTACTTCAGCCCTATAACAA
 AACTCACATATATGTGTGGAACTGGAGCATTCATCCAATATGTGGGTATTGATCTGGAGTCTACAAGGA
 GGATATTATATTCAAACACTAGACACACATAATTGGAGTCTGGAGACTGAAATGTCCTTGCATCCTCAGCAGCC
 TTTGCTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTCTGATTCCTGGCAAAGATACTGCATT
 CACTCGATCCCTGGGCCTACTCATGACCACCATACATCAGAACTGACATTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTATTGGAACCTTCTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTTCTTCTG
 TGAATCATCTAAGAAGGCAGTACCTCCGATAAAACCATCCTTCTGAGTTGGAGAGTTGTAAGAATGATGT
 AGGAGGACAACGCAGCCTGATAAACAAAGTGGACGACTTCTTAAGGCCAGACTGATTGCTCAATTCTGGAAAG
 TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTATTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGCTTACTACAACCAGCTCCATCTCAAAGGCTGCTGTTGTTGATAGCATGGCTGACAT
 CAGAGCAGTTTAATGGCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCACTGATGAGGGAGAAT
 TCCTTATCCACGGCTGGTACATGTCAGCAGAAACCTATGACCCACTGATTAAGTCCACCCAGGATTTCAGA
 TGATGTCATCAGTTCTAAAGCGGCACTCTGTGATGTATAAGTCCGATACCCAGTTGCAAGGAGGACCAACGTT
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGGAGTATGTCATTGCAAGAGATGCCAGTACGA
 TGTAATGTTCTGGAAACAGACATTGGAACTGTCTCAAAGTTGTCAGCATTCAAAGGAAAGTGGAAATATGGA
 AGAGGTAGTGTGGAGGGAGTTCAGATATTCAAGCACTCATCAATCATCTGAAACATGGAATTGTCCTGAAGCA
 GCAACAATTGTCATATTGGTCCCAGATGGATTAGTCAGCTCTCCTGCACAGATGCGACACTATGGGAAAGC
 TTGGCCAGACTGTTGTCAGAGACCCCTACTGTCGCTGGGATGGAATGCACTGCTCTGATATGCTCCTAC
 TTCTAAAAGGAGAGCTAGGCCAAGATGTAAAATATGGCAGCCAACTCACCCAGTGCTGGGACATCGAAGACAG
 CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTGGCATTGAAATTCAACTCCTTCTGGAATGTATACC
 TAAATCCAAACAAGCAACTATTAAATGGTATATCCAGAGGTGAGGGATGAGCATCGAGAGGAGTTGAGGCCGA
 TGAAAGAATCATCAAACCGAATATGGCTACTGATTGAGTTGCAAGAGAAGGATTCTGGGATGTTACTG
 CAAAGCCCAGGAGCACACTTCATCCACCCATAGTGAAGCTGACTTGAATGTCATTGAGAATGAACAGATGGA
 AAATACCCAGAGGGCAGAGCATGAGGAGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
 CTACATCCAAATCCTAGCAGCCAAACTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG
 GAGACAGAGAAACAAGGGGGCCAAAGTGGAAAGCAGATGAGGAATGAAGAAGAACGAAATCGAACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGAGCCACG**T****A**GTTTCTACTTAATTAAAGAAATTCTTAC
 TATAAAAACATTGCTTCTGTTTGATATCCCTATAGTAATTCTAAATGCTCCCATGGAGTTTGCTAAGG
 CACAAGACAATACTGAAATAAGACAATATGTGATGAATATAAGAAGGGCAAAATTCTGAAACCAGTTT
 CCAAGAACAAATCTGACAAGCAAGTATAAGAATTATCCTAAAAATAGGGGTTACAGTTGTAATGTTA
 TGTTTGAGTTGGAAATTATGTCATGTAATAGTGGCTAAGCAAGGCCAATTGATAGTGTATAAGGT
 GCTTTATTCCCTCGAATGCTCCTTAAGCATGGAATTACCATGCGAGTTGCTATGTTCTTATGAAACAGATAT
 CATTCCTATTGAGAACCGACTACCTGTGGTAGGGATAAGAGGTGAGCACACAAATTAAAGACAACCTCCATTAC
 AACAGGAACCTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTGGAGAGGTGCAATTGTT
 TGCCACTGGGTTAAATTAGTGTACTACAAACATTGATTACTGAAGGGACTAATGTTCCCCCAGGATTCT
 ATTGACTAGTCAGGAGTAACAGGTTCACAGAGAGAAGTTGGTCTAGTTATGTTTTAGAGTATATACTAA
 GCTCTACAGGGACAGAATGCTTAATAAAACTTTAATAAGATATGGAAAATTGTTATAAAACAAGGAAACAA
 TAATGATGATAATGCATCCTGATGGGAAGGCATGCGAGATGGGATTGTTAGAAGACAGAAGGAAAGACAGCCAT
 AAATTCTGGCTTGGGAAAACCTCATATCCCATGAAAAGGAAGAACAAATCACAAATAAAAGTGAGAGTAATGAA
 TGGAGCTCTTCACTAGGGTATAAGTAGCTGCCAATTGTAATTCTGTTAAAAAAATCTAGATTATAACA
 AACTGCTAGCAAAATCTGAGGAAACATAAATTCTCTGAGAACATAGGAAGAGTAGACATTATTATAACC
 AATGATATTCTAGTATATATTCTCTTTAAAAAATATTATCATACTCTGTATATTATTCTTTACTGC
 CTTTATTCTCTCTGTATATTGGATTTGTGATTATTTGAGTGAATAGGAGAAAACAATATAACACACAGA
 GAATTAAGAAAATGACATTCTGGGAGTGGGATATATTGTTGAATAACAGAACGAGTGTAAATTAAAC
 AACGGAAAGGGTTAAATTAACTCTTGACATCTCACTCAACCTTCTCATTGCTGAGTTAATCTGTTGAATT
 GTAGTATTGTTTGTAAATTAAACAATAAGCCTGCTACATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPTGTLKQNI PRLKLTYKDLLLNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAKDHFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLSGTASDFLGKDTAFTRSLGPTHDHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTS DKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPV VYGVFTTSSIFKGSACVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVVDYRLTQIVVDH VIAEDGQYDVMFLGTDIGTVLKVV SISKEKWNMEEVVLEE
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQA
TIKWIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKD YIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRRHHRDLDLPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTTGGAAAGCCGCAGAGGTATCCTGGAGCATGCCACCAGCGGGGAGCAGA
 CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTCTCAGGAGCCTGGTGTATTTCACCCACCCCCAC
 CTCAGCAGTTCAGCCACAGGGACTGATCAGGTGTGTCTGGAGTGGGAGCAGAAGGCCTGGCTGGCAAGA
 GTGGCCTGGAGAAAGAGGTTCAGCGCTTGACCAGCCAGCTGCCCTGACTACAAGATCCAGAACCATGGGCATC
 GGGTGAGGTGGGGGGCACAGGTGTATGTGACCTCTGTCTCAGCAAGAAGAGCTGAGAGAGGGATCTGG
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGAGGGAAAGGTATTTAAGGTAACAGTGTGGCACAATAGTTAA
 GAGCACAGTTTGGAGCTAGACCGACATAGGGTCAAATTCTCTGTTGCTTAGTCTGTAGCCCCAGGT
 AAGGGAGTGACTTAACCTCTGGACTTCATACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
 AGGGAGATAATGACATAATGTATGT**G**TA**C**AACTAGCAAAGTACCAAGTCCCATAGTAAGTCA
 TATTCACCCACCCCTGTTCTGCTGCCCTCCAAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT
 CAGAGCGGGAGGGCTCAAGCATAAGAACAGAGGTTACAGGAAGTGCAGAGAGACATCCGCCGGGACAGGTGAGCC
 AGGTGAAGGGGGCTGCCGGCTGGCCCTGCTGCAGGGGGCTGGCTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGGCGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTC
 CAACCGCTGAGGATGCTGAGCTTCTGACTTGAGGAATGTGAGGAGACGGGAGAGCTCTTGAGGAGCCTGCC
 CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTCGCTATCAGGAGGGCTGAGGATG
 AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTATAGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
 ACCAGCACGGCGAGGTAGGCTTGTCCCTGAGCGATATCTCAACTTCCCGACCTCTCCCTCCAGAGAGCAGCC
 AAAGACAGTGACAATCCCTGCGGGGAGGCCACAGCATTCTGACAGGACCTGTACAGTACACCGGACAGA
 GTGCAGAGGAGCTGAGCTCCCTGAGGGGGACTCATCCGTCTGCTGCCCGGGCCAAAGATGGAGTAGATGACG
 GCTTCTGGAGGGGAGAATTGGGGGCCGTGTTGGGTCTTCCCTCTGCTGTTGGAGAGGCTTGGCTTGGGGGG
 CAGGGCCACCTGAACTCTGACCCCTGAACAGATGCTGCCGTCCTCTCCCTCCAGCTTCTCCCCACCTGCAC
 CTACCTCTGTGTTGGATGGGGCCCTGACCTGTCCCTGGGACAAAGCCCTGGACTTCCCTGGGTTCTGG
 ACATGATGGCACCTCGACTCAGGCCATGCGTCCACCCACCTCCCGGGCTAAAGCCCCGGATCCTGGCACC
 CAGATCCCCTACCT**TG**AAAGGCCAGGGAAAGCCTGACCCCCAGTGTGCTGCTGCCCTATCTCAAGCTGT
 CAGA
 CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATGCCCTTATTTCACCCCTCACCTCAAGGGT
 GGAAACTTGCCCCCTCCATTCTAGAGCTGGAACCCACTCCTTTTCCATTGTTCTATCATCTAGGACC
 GGAACTACTACCTTCTCTGTCTGATGACCTATCTAGGGTGGTGAATGCCCTGAAATCTCTGGGCTGGAAACC
 ATCCATCAAGGTCTCTAGTAGTTCTGGCCCACCTCTTCCCCACCCCTGGCTCCATGACCCACCCACTCTGGATG
 CCAGGGTCACTGGGTTGGCTGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGGCCAGGATGCGAAGCAG
 CTGTAATGGCTGAGCGGATTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCTGGCTTGTG
 CTAAGAGGGCAGGGGCCACGGTGTATTGCTTAGGGGCCACACGGGAGGGCTGCTCCAGTGCAC
 GCTCTATCATATGGAGCGAGGTGTTGGGAAGGCAGGGCAGGCAGCTGTTGCAAGGAGGGAAAGGAGAAGAC
 TGAGGGCTGTGACCTCTCTGAGGCCAGGCTGAGACTGTGCAACTCCAGGTGGAAAGTAGAGCTGGTCCCTC
 AGCTGGGGGGCAGTGTGTCAGTGGAGGGAGGGCTTACGCCACCCACCCCTGGCCCTGCCAGTGGTAG
 TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGATAACACTGTTGCTCTGTTCAAGCTGTGTCAGC
 TTTCCCTGGGCTCCAGGACCTCCCTACCTCACCAACCAAGGGATTATAGCAAAGGCTAACGCTGC
 AGTTTACTCTGGGGTTCAAGGAGCCGAAAGGTTAAATAGTTAAGTAGGTGATGGGAAGATGAGATACCTCA
 TTTAGGGCTCAGGCAGACTCACCTCACACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGG
 TCAACAATGAGAGACCCAGGAGTAGGTCTCTATCAGTGCCCCCAGAGTAGAGAGGAATAAGAGGCCAGCCAGTGC
 AGTCCCCGGCTGTGTTCTACCTGGTGTACGAAAGTGTCTGGTTGCTGGCTGCCATTGCTCTGAGTGG
 GCAGGCGCTGGCTGGGCCCTCCCTGGGCCCTCAGTGTGGCTCAGAAGCTCTGGGTTCCCTCAAGTG
 CACGAGGGGTTAGGCTGCTGCTGCCATTCTGAGTCCTCAGTGTGCTGAGGAGCTGGCTAGGACCTGGGCTGTGGCC
 TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCTGCCTGGCTGCCCTCCCCAGACCCCTGACCACCCCTG
 GGTCTGTCCCCCACCAGAGCCCCAGCTCTGTGTGGGGAGGCCATCAGGTGTTGCTGAGTCCATAGCGCT
 TCTCAATGTGTGTCACCCGGAACCTGGAGGGAGGGAAACACTGGGTTAGGACCAACTCAGAGGCTGTTG
 GCCCTCCCTCTGACCAAGGGACATCCTGAGTTGGCTACTCCCTCTGGCTAAGGTAGGGAGGCCCTCTC
 AGATTGTGGGGCACATTGTGAGGCTGACTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT
 TTGGGATCAGGTGCTGATCACTGGGCCCTACCTCAGCCCCCTTCCCTGGAGCACCTGCCACCTGCCCA
 CAGAGAACACAGTGGCTCCCTGTCGGGGGGCTTTTCCCTGGAGGCGTCCCTGACGGACAAGTGGAG
 GCCTCTGCTGCGGCTGCAATGGATGCAAGGGCTGCAGAGGCCAGGTGCACTGTGATGATGGAGGGGCTC
 CGTCCTGCAAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGAGTGGAGGTAACATTCCATT
 TCATGTTGTTCTACGTTCTCAGCATGCTCTTAAACCCAGAACGCCAACCTCCAAAGGCCATT
 TTTCTGTCTTATCTAAATAACTCAATATTAG

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTTGEWEVIEEGDADEW
VKARNQHGEVGFPERYLNFPDLSLPSESSQDSDNPCGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVVDDGFWRGEFGGRGVVFPSLLVEELLGPPGPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPAKAPDPGHPDPLT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGAAAGAGACAGAGACAAAGGCACAGCGGAA
 GAAGGCAGAGACAGGGCAGGCACAGAACAGCGGCCAGACAGAGTCCTACAGAGGGAGAGGCCAGAGAACGTCAGA
 AGACACAGGCAGGGAGAGACAAGATCCAGGAAGGGACTCAGGAGAGAGTTGGAGAGGCCAGACCCCTGG
 GCACCTCTCCCAGGCCAAGGACTAAGTTCCTCCATTCTTAACGGTCTCAGCCCTCTGAAAACCTTGCC
 TCTGACCTTGGCAGGAGTCAAGCCCCCAGGCTACAGAGAGGACTTCAAAGCTAGGGTGTGGAGGACTTGGT
 GCCCTAGACGGCTCAGTCCCTCCAGCTGCAGTACAGTGCATGTCCCAGACAGGCTCGCATCCGGGAGGGG
 CTTGGCAGGGCCTGGCTGGGGAGCCAACCCCTGCCCTCTGCTCCCCATTGTGCCGCTCTCCTGGCTGGTGTG
 GCTGCTTCTGCTACTGCTGGCTCTCTGCCCTCAGCCGGCTGGCCAGCCCCCTCCCCCGGGAGGAGGAGAT
 CGTGTTCAGAGAACGCTAACGGCAGCGTCTGCCCTGGCTGGGCCAGGCTGTTGTGCCGCTTGCA
 GGCTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTGAGGGGCTGACAGTGCAGTA
 CCTGGGCCAGGGCCTGAGCTGCTGGTGGAGCAGAGCCTACCTGACTGGCACCATCAATGGAGATCC
 GGAGTCGGTGGCATCTGCACTGGATGGGGAGGCCCTTAGGCGTGTACAATATCGGGGGCTGAACCTCCA
 CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACACTGCTGGGGACCTGGGCTCACATCCTACGCCGAAGAGTCC
 TGCCAGCGGTCAAGTCCATGTGCAACGTCAAGGCTCCTTGAAGGCCAGGCCAGACCCGAAGAGCCAA
 GCGCTTGCCTCACTGAGTAGATTGTGGAGACACTGGTGTGGCAGATGACAAGATGCCGATTCCACGGTGC
 GGGCTAAAGCGCTACCTGCTAACAGTGTGGCAGCAGCAGGCCAAGGCCCTCAAGCACCCAGCATCCGAATCC
 TGTCAGCTTGGTGGTGAECTGGCTAGTGTGCTGGGGTCAAGGCAGGGGCCCAAGTGGGGCCAGTGC
 CCAGACCCCTGGCAGCTCTGTGCCAGGGGCCCTAACACCCCTGAGGACTCGGGCCTGACCACATTG
 CACAGCCTTCTGTTACCGTCAGGACCTGTGGACTCTTGAACAGCCTTGTGGTATGGCTGATGTGG
 CACCGCTGTGACCCGGCTGGAGCTGTGCCATTGTGGAGGATGTGGCTCCAGTCAGCCCTCACTGCTGCTCA
 TGAACGGTGTGATGCTTCAACATGCTCCATGACAACACTCCAAGGCATGTCATGCTTGAATGGGCTTGTGAC
 CTCTGCCATGTCATGGCCCTGTGATGGCTCATGTGGACTCTGGGACTGGTCCCTGAGTGGCCCT
 CATCACTGACTCTCTGGACAATGGCTATGGCACTGTCTTAGACAACACAGAGGCTCCATTGCA
 GACTTCCCTGGCAAGGACTATGATGCTGACGCCAGTGCAGCTGACCTCGGGCCACTACGCCATTG
 ACAGCTGCCGCCCTGTGCTGCCCTGGTGTCTGGCACCTCAATGGCATGCCATGCCCCAAC
 CTCGCCCTGGCGATGGCACACCCCTGGGCCACAGGCCATGGTGGTGTGCTGCCCTCACATGGACCA
 GCTCCAGGACTCAATATCCACAGGCTGGTGGCTGGGACCATGGGTGACTGCTCTGGACCTG
 TGGGGTGGTGTCCAGTCTCTCCCGAGACTGCACGAGGCCGTGCCCCCGGAATGGTGGCAAGTACTGTGAGGG
 CGCCGTACCGCTTCCGCTCTGCAACACTGAGGACTGCCAAGTGGCTCAGCCCTGACCTTCCGGAGGGAGCA
 GTGTGCTGCCATAACACCACGCACCGACCTCTCAAGAGACTCCCAGGGCCATGGACTGGGCTCTGCTACAC
 AGGCGTGGCCCCCAGGACCACTGCAAACACTCACCTGCCAGGCCGGACTGGCTACTACTATGTGCTGGAGCC
 ACGGGTGGTAGATGGACCCCTGTCCCCGGACAGCTCTGGTGTGTCAGGGCGATGCA
 CTGATGCAATTGGCTCCAAGAAGATTGACAAGTGCATGGTGTGCGGAGGGACGGTTCTGGTTGCAG
 CAAGCAGTCAGGCTCTTCAGGAAATTAGGTACGGATAACAATGTGGTCACTATCCCCGGGGGCCACCCA
 CATTCTTGTCCGGCAGCAGGGAAACCCCTGGCACCGGAGCATCTACTTGGCCCTGAAGGCTGCCAGATGGCTCCTA
 TGCCCTCAATGGTAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGCA
 CAGCGGGGCCACTGCAGCTCAGAGACACTGTCAGGCCATGGCCACTGGCCAGCCCTTGA
 ACTGCAAGTCCT
 AGTGGCTGGCAACCCCGAGGACACACGCCTCCGATACAGCTTCTCGGCCCCGGCAGCCCTTCAACGCCACG
 CCCACTCCCCAGGACTGGCTGACCGAAGAGACACAGATTCTGGAGATCCTCGGCGGCCCTGGCGGGCAG
 GAAATAACCTCACTATCCGGCTGCCATTCTGGCACGGGGCTCGGACTTAGCTGGAGAAAGAGAGAGCTT
 CTGTTGCTGCCCTATGCTAAGACTCACTGGGAGGGCTGTGGCGTGGAGACCTGCCCTCCTCTGCCCTAAT
 GCGCAGGCTGCCCTGCCCTGGTTCTGCCCTGGGAGGCACTGGGACTGAGACCTGCCCTCCTCTGCCCTAAT
 AGCCCTCCATCTAAACTGCCCTCTGCCCTGCCCTGGGACTGAGGAGGGGACAAGGACTAGGGTCTGGGAA
 CAGTTGATTATTAGTATTACTTATTAGCACCAAGGGAGGGGACAAGGACTAGGGTGTGATAGGTATAAGTGGT
 TGTGATGCGTGTGTGTGTTGAAAATGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCC
 TTCTGTAATTATTAGGAAAGAAAAGAACAGTCAAGGGTAGGGTGGGCCCTCAGGGAGTGGAGGATTATCTTT
 TTTTTTTCTT
 GCACAATCTGGCTCACTGCATCCTCCGCCCTGGGCTCAAGTGTGATTCTCATGCCCTCAGCCTCCTGAGTAGCTG
 GGATTACAGGCTCCTGCCACCAGGCCAGCTAATTGGTTGTTGGAGACAGAGTCTCGCTATTGTC
 ACCAGGGCTGGAATGATTCACTGCAACCTTCGCCACCTGGGTTCCAGCAATTCTCTGCCCTAGCCTCC
 CGAGTAGCTGAGATTATAGGCACCTACCACGCCAGGCTAATTGGTGTATTAGTAGAGACAGGGTTTCAC
 CATGTTGGCCAGGCTGGCTCGAACCTGACCTTAGGTGATCCACTGCCCTCATCTCCCAAAGTGTGCTGGGATT
 ACAGGCGTGAGGCCACCGTGGCACGCCAACTAATTGGTATTAGTAGAGACAGGGTTTACCATGT
 TGGCCAGGCTGCTCTGAACTCCTGACCTCAGGTAATCGACCTGCCCTGGCCTCCCAAAGTGTGCTGGGATTACAGG
 TGTGAGGCCACCACGCCGGTACATATTAAATTGAAATTCTACTATTATGTGATCCTTGGAGTCAGACAG

FIGURE 179B

ATGTGGTTGCATCTTAACTCCATTGTCAGCATTAGATTTCTCATTTGCCAATAATAACCTCCCTTAGAAG
TTTGTGAGGATTAAATAATGTAATAAGAACATGCAACACTCAAAAAAAAAAAAAAAA
AAAGGAAA

FIGURE 180

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASLLPSARLASPLPREEEIV
FPEKLNLSVLPGSGAPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTGTINGDPESVASLHWDGALLGVLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRRAKRFAISRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAKHPSIRNPVSLVVTRLVILGSGEEGPVQVGPSAAQTLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHD
NSKPCISLNGPLSTSRRHVMAPVMAHVDPPEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFPGKDYDADRQCQLTFGPDSRHCPCQLPPPACAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTCAGGGVQFSSRDCTRVPVRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFYGYNNVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPQDWLHRRAQILEILRRRPWAGRK
```

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
 CAAAGAACCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTAAATCC
 AAGAAAATATGTAAATCACTTAAGATTGTGGACTGGTGTTCCTGCCCTAACTCT
 AATTGTCCTGTTGGGGAGCAAGCACCTCTGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTG
 ACCAGAACTGAAATATTCAAGCGGAAATGGCACTGATGAAACATTGAAAGTGCACGACTT
 TAAAAACGGATACTGGCATCTACTTCGTGGTCTTCAAAATGTTATCAAAACTCAGA
 TTAAAGTGATTCTGAATTTCTGAACCAGAAGAGGAATAGATGAGAATGAAGAAATTACC
 ACAACTTCTTGAAACAGTCAGTGATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTCTTAAAAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTCTGAGTTACAAGACTTGAGGAGGGAGGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCGTCACGCCAGACAAGCAAGTGAGGAAGAACCTCCAATAATGACTATACTG
 AAAATGGAATAGAATTGATCCCATGCTGGATGAGAGAGGTTATTGTTGATTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCTGTGAACCTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGCGTGTACATGCCCTGTAAGTGGTGGTGGCCC
 GCATGCTGGGAGGGTCTAATAGGAGGTTGAGCTAAATGCTAAACTGCTGGCAACATAT
 AATAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT
 CTCCAGAATTACTGTAGGTAATTCTCTCTTCATGTTCTAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTTLIVLFWGSKHFWPEVPKKAY
DMEHTFYSGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEETTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHF PAN EKKGIEQNEQWVV P QVKVEKTRHARQASEEELPINDY
TENGIEFDPM LDERGYCCY CRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCAGGAACCTGGCTCCGGCTGGCACCTGAGGAGCAGCGTGACCCCGAGGGCCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCGTGCAGCTCTGGCTTCCT
 GCTCAGCTTCTGGGCATGGTGGGCACGTTGATCACCAACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCGTGTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCGCCCTCATGGTCATCTCCTGCCTGCTCTGGGCATAGCCT
 GCGCCTGCCGTACGGATGAAGTGCACGCCGCTGCCAACGGCACACCCGCCAAGACC
 ACCTTGCCATCCTCGCGGCACCCCTTCATCCTGGCCGGCCTCTGTGCATGGTGGCGT
 CTCCCTGGACCAACGACGTGGTGAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGCTCATCTCCTCGCCCTCGCTCATTGGT
 GGCACCCCTGCTTGCCCTGCGCAGGACGAGGCACCCCTACAGGCCCTACAGGCCCGCC
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCTGGCTGCTGTGGCTGGTCCCCGGCGGACTGTC
 AATGGAGGCAGGGTTCCAGCACAAAGTTACTTCTGGCAATTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTAGAGGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAATCCTGTCTGTTTGATTTATTATATAT
 TTATGTGGGTGATTGATAACAAGTTAATATAAGTGACTTGGAGTTGGTCAGTGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGGGATGTGGCTGTTATGAAAAAAAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAWSWTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLISLIGTLLCLSCQ
DEAPYRPYQAPPRATTTANTAPAYQPPAAYKDNRAPSVTSAHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCTCAGGAGCGCGTTAGCTCACACCTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCAGGGCGGCCAGGAT**ATG**TCCACCACATGCCAAGTGGTGGCGTTCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGCCACCAGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCGTCACCTCCGTGTTCCAGTACGAAGGGCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTCACCGAATGCAGGCCATTTCACCATCCTGGACTTCCAGC
 CATGCTGCAGGCAGTGCAGGCCATTGATGATCGTAGGCATCGCCTGGTGCCATTGCCCTCC
 TGGTATCCATCTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTGCAATTGCTGGAGT
 GTCTGTGTTGCCAACATGCTGGTACTAACTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTGGTGCGGCTCTGTTCGTG
 GGCTGGGTGCGTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGG
 CCTGGCACCAAGAAACCAACTACAAAGCCTTCTTATGCCTCAGGCCACAGTGTG
 CCTACAAGCCTGGAGGCTCAAGGCCAGCACTGGCTTGGTCCAACACCAAAAACAAGAAG
 ATATACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTTATCCTCCAAGCACGACTA
 TGTG**TAA**TGCTCTAACACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTACCCAAA
 AACAAAGGAGATCCCCTAGATTCTTGCTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTCATCTTGGAGAGGCCAAATGGTCTAGCCTCAGTCCTGTCTCAAATATTCC
 ACCATAAAACAGCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTCAATCCTCTAT
 TTCTTTTTAAATATAACTTCTACTCTGATGAGAGAATGTGGTTTAATCTCTCTCAC
 ATTGATGATTAGACAGACTCCCCCTTCCCTCTAGTCATAAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCCAAGAAAATTGAAAGGAAAGAGTAGACCCAAAGATGTATT
 CTGCTGTTGAATTGTCTCCCCACCCCAACTGGCTAGTAATAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTGTAATCTCCAGCCATGATCTGGTTTCTTACACTG
 TGATCTAAAAGTTACCAACCAAAGTCATTTCAGTTGAGGCAACCAAACCTTCTACTG
 CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAG
 TCCTCTTCTGCGGGTCAGAAATTGTCCTAGATGAATGAGAAAATTATTTTTAAT
 TTAAGTCCTAAATATAGTAAAATAATGTTTAGTAAAATGATACTATCTCTGTGA
 AATAGCCTACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGTCT
 ATATGGTACTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTGGAGGCTGAGGAGGAAGGATCACTTGAGGCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGCTCTACAAATAACAGAGAGAAAAATCAGCCAGTCATGGT
 GCATACACCTGTAGTCCCAGCATTGGAGGCTGAGGTGGAGGATCACTTGAGGCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAATAAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
 ACTAATTCTTAA

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSFVANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAAACTGTTCTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTCCG
 GAGTCCAGCTGGCTAAAACATCCCAGAGGATA**ATG**CAACCCATGCCTAGAAATCGCTG
 GGCTGTTCTGGTGGTGGAAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
 CTCTTCTCCGGACCTACAGGCAGGCCAGAGGACTGATGTCATGCTCCGTGATGTCCTTC
 TTGGCTTCATGATGGCCATCCTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCATCACGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGTTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT
 GTGCCCAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACACGGCACTGGTGC
 GATTGTTGGAGGAGCTGTTCTGCTGCGTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTATGTTTTAACTTTACTATAAAGC
 CATGCAAATGACAAAAATCTATATTACTTCTAAAATGGACCCAAAGAAACTTGTATTA
 CTGTTCTTAACTGCCTAATCTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTCAGCAGAATGAGATATTAAACCAATGCTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTCTAAGGTGGTCAAGCATCTACTCTTTATCATTACTTCAAAATGACATTGCT
 AAAGACTGCATTATTTACTACTGTAATTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTATCTCACATAGAGACATGCTTATGGTTATTAAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTCAGGGAAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTAAAACAGCTAGGGATTATGCTCCATTATAATGA
 AGATTAATGAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG
 TTTTTAGCCTAGGAGTTAGAAATCTAACCTCTTATCCTCTCCAGAGGCTTTT
 TTCTGTGTATTAAATTAACATTCTAAAACGCAGATATTGTCAGGGCTTGCATTCA
 AACTGCTTTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTG
 GTTTAGGAAAGTGAAAAATTGGTTTGTATTGAAGAAGAATGATGCATTGACAA
 GAAATCATATATGTATGGATATTAAATAAGTATTGAGTACAGACTTGGAGGTTCATC
 AATATAAATAAAAGAGCAGAAAAATATGTCTGGTTTCATTGCTTACCAAAAAACAACA
 ACAAAAAAAAGTTGCTTGTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTC
 ATTTGTTCTGTGAAAATAAATTCTCTGTACCTGCTTACCAATTCTGTTAGTTACTAAA
 ATCTGTAAATACTGTATTCTGTTATTCAAATTGATGAAACTGACAATCCAATTG
 AAGTTGTCGACGTCTGTCTAGCTAAATGAATGTGTTCTATTGCTTATACATTATA
 TTAATAAATTGTACATTCTAATT

FIGURE 188

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSIFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTLVLIVGGAFFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGCTGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTCATCGAACAGCAT
 CGTGGTGGCCCAGGTGGTGTGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTCATGCCCTCCTGTGGCCCTGTCGGCTGCTGGTCTACCTGCTGGGC
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCGCCTGGTGCACCTCTGGGA
 TTGTCTTGTCATCTCAGGGCCTGACGCTAATCCCCGTGCTGGACGGCGATGCCATC
 ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCAAAAGCAGGGAGCTGGGGCCTCCCT
 CTACTTGGGCTGGCGGCCTCAGGCCTTTGTTGCTGGTGGGGTTGCTGTGCTGCACCT
 GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCT
 GCCATCTCTCGGGGGCCCTTGAGTACCCCTACCAAGAATTACGTCTGACGTGGAGGGAAATG
 GGGGCTCCGCTGGCGCTAGGCCATCCAGAAGTGGCAGTGCCAACAGCTTGGATGGGTT
 CGTACCTTTGTTCTGCCTCTGCTATTTCTTGACTGAGGATATTAAAATTCAATT
 GAAAAGTGGAGCCAAGGTGTTGACTCAGACTCTCACCTAGGCTCTGCTGTTCTCACCCCTGG
 ATGATGGAGCCAAAGAGGGATGCTTGAGATTCTGGATCTGACATGCCATCTAGAACG
 CAGTCAAGCTATGGAACTAATGCGGAGGCTGCTGCTGGCTTGCACAAAGACAGAC
 TGTCCTCAAGAGTTCTGCTGCTGGCTGGGCTCCCTAGATGTCAGGGACTG
 CCCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTTCACCCCTGGAAAAACAAATCATCTG
 TTAACAAAGGACTGCCACCTCCGGAACCTGACCTCTGTTCTCCGTCTGATAAGACG
 TCCACCCCCCAGGGCCAGGTCCCAGCTATGAGACCCCCGCCACCTCCAACACTGCACC
 CTTCTGCCCTGCCCTCGTCTACCCCTTACACTCACATTATCAAATAAGCATG
 TTTTGTAGTGCA

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLG WVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTS
FVISGVLTLLIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLGGGLCCTCP
SGGSQGPGSHYMARYSTSAPAISRGPSEYPTKNYY
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAAGGCTCCACGTTCTACATCTTG
AGCATCTTCTACCACCTCGAATTGAACCAGTCTCAAAGTAAAGGCAATGGCATTATCCC
TTGCAAATTGCTGGGCTGGTCTTGGGCTTGGCATGGTGGGACTCTGCCACAACCC
TCTGCCTCAGTGGTGGAGTATCAGCTTGTTGGCAGCACACATTATTGTCTTGAGAGGCTC
TGGGAAGGGCTCTGG**ATGA**ATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
TAGCTCCTTGGCTCTCCGCCTGCCCTGGAAACAGCCCAGGGCCCTCATGTGTGGCTG
TTGCTCTCCTTGATGCCCTGCTTATTGGCATCTGGCATGAAGCAGGTCCAGTCACA
GGCTCTAACGAGAGGGCAAAGCATACTTCTGGAACTTCAGGAGTCCTTCATCCTGAC
GGGTATCTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
ACCCAGCCATCCACATAGGTAGAACAGAGACTGGAGCAGCACCTTCCTGGCTGGCA
AGCGCTGCTGTCCTCTCATTGGAGGGGTCTGCTTGTGGATTTGCTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCACCAGTTATGTC**TAA**TGCCTCCTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
GAACTTGCTTATGTCTAGATTACATTGATACGAAAGTTCAATTGTTACTGGTGGTAGG
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG
GACCCAATCGCTGCTCCAATTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
TGTACAATGATGGACTACTTATTACTTTGACCATCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAACATACCTATTCTA

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRKKQGYRYPVPGYRPHTDKRRNTTMLSKTSTSYV
```

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGC**ATG**AAGATCACTGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTACAAGAAGTATCCAGTGGTGGCCATCCCCATGCCCATCA
CATACCTACCAGTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAAGAGTAATCTTG
ACTGAATGGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCGCAT
TTTTTTTTAACACGTCAATAAAAAATAATCTCCCAGA

FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCAGCCCCTGCCCTCCTGCTCGCGCCC
CGCCGCCATGGCTGCCTCCCCCGCGGGCTGCTGTCCTGGCCCTGACCGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGCCAGGTGGCATAAGTGGAAATAACTCAAGCTGATGCTCAA
AACGAGAAGCACCTGTTCCAACTAAGACTAAAGTGGCGTTGATGAGAATAAGCAAAGA
ATTCCCTGGCAGCCTGAAGGCCAGAGCGGAGCTGTGGACCGACTCGGCCGAGGTGC
AGCAGTGGTACCAGCAGTTCTCATGGCTTGATGAAGCAAATTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTAACCATGACTGCCACACGCTGTACAAGCAAATAGCGATT
TCTTCATGTATCTCCTAACGCCTTACACTACTGGTTCTGATTGCTCTATTCAGCAGAT
CTTTCTACCTACTTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTT
TGATATTCATGGGAATGCCTCTCATTAAAAATAGAAATAAGCATTGTTAAAAAGA

FIGURE 196

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLCWGPAGISGNKLKMLQKREAPVPTKTKAVDENAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYGDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY
```

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCGCCGGAAAGTCCCCGAGGGGCCGCGATGGAGCTGGGGAGCCGGCGCTC
 GGTAGCGCGCGGGCAAGGCAGGCATGACCTGATTGAAGGGTGGGTATGAGGTGAC
 CGTCCTTTCTCGGTGCTTGCTGCCTCTGGTGCCTGGCCCTGGCTGGTCTAACGCACA
 CCGCTGAGGGCGGGACCCACTGCCAGCCGTAGGGACCCAACGCCATCCCAGCCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCCCAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGGCCAGCACGGGTTCACAGAACACCGCCAG
 CCCCAGACTCCCCGAGGAGCCCTCGTGCCTGAAATTCCCTCAATGATTAGCAGAGCAG
 GTGGCCAGGGCTGGCCCCACGACACCATTGGCTCCTGAAAAGGACCCAGTTCCGGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCAGCACCCAGACCCCTGG
 GCAGCCTTCACCTCCCTCCAACTGCCTCTCCACTGCCACGTGTCACGAGAGTCGGTCCC
 CCAAATCCCCCTGCCGCCGGGTCCGAGCCGCCCTCCGGGCTGGAAATGGCAGCCT
 GCTGCTGCCCTGCTCCTGCTGTTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
 CCTTCTTCCCTGACCGCCACTCTGGCCTGCCGGCTCACCTGCTCCTCAGTCTCCTG
 GCCTTGCCATGTACCGCCG**T**AGTGCCTCCGCCGGCGCTGGCAGCGTCGCCGGCCCTCC
 GGACCTTGCTCCCCGCCGCCGGAGCTGCTGCCAGGCCCTCCGGGCTCAGGCCCT
 CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCCCGCAGAGGACTCCGGGACTGGGGAGG
 CCCGCCCTGCGACCGCCGGGCTGGGGCACCTCCGGGCTGCTGAACCTCAGCCGCA
 CTGGGAGTGGGCTCCTCGGGTGGCATCTGCTGTCGCTGCCCTGGCCGGCAGAGCCG
 GGCGCCCCGGGGCCGTCTAGTGTGCTGCCGGAGGACCCAGCCGCCTCCAATCCCTGAC
 AGCTCCTGGCTGAGTTGGGACGCCAGGTGGTGGAGGCTGGTAAGGGAGCGGGGAG
 GGGCAGAGGAGTTCCCCGGAACCGTGCAGATTAAAGTAACGTGAAGTTAAAAAAAAA
 AAAAAAAA

FIGURE 198

MTLIEVGDEVTVLFSLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRILYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLWYCQIQYRPFFPLTATLGLAGFTLLLSSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCCTCCCCCTCCAAGG**ATG**ACAAAGGCGCTACTCATCTATTGGTCAGCAGC
TTTCTTGCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGG
AAAGCAAGTTCAACATATCAAAGATAATGAAAATGCGGATGGAAGCTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGAACGATTATAAGAGTTACTCGGAAAACCTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCAACCTTCTGCAGGCATCCACTGCGAAAAAGGA
TTGTGTCCGGAGCACGGGGATGAACAACACTGGGTAGAATGGAGGTTGCACTGTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCTGAGA**TGA**AACAGGGTGCAGGTGCACCGTGG
AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTTCATTTCCTTCCACTGCCTCCA
CTTCATGTTATTTCTCCCTCCATTACAACAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTCTGGCTCCTCCTACTCCCCTGACCCAGTCCCTGGTTCTGTCTGTTAT
TTGTAACACTGAGGACCACAATAAGAAATCTTATATTATCG

FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSSENLCHVDCQDLLNPNLLAGIHCARKIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATTATTTTCCCAAGGAGAAAACCGGGTAAAGGGAGGGAAGCAATT
 AATTGAAGTCCCTGTGAATGGGCTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
 TTGGGTGAAACTTGGGTCTGTGGTTCTGATTGTAAGTGAAGCAGGTCTGCACACGC
 TGTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAAACTCCAGGTGGAACAAGCA
 ACCATGTTCTGCTGCAAGCTGAAGGAGCCTGGAGCAGGAGAAAGCTAACATTGAACATGAC
 CTGTTGCATTGGCAAGTTCTAGCAAC**ATG**CTCCTAAGGAAGCGATAACAGGCACAGACCATG
 CAGACTCCAGTTCCCTGCTGCTCCTGATGCTGGATGCGTCCTGATGATGGTGGCGATGT
 TGCACCCCTCCCCACCACACCCCTGCACAGACTGTCACAGCCCAAGGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTGGGAATCCCAGGATTGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCGTGGCCTACCCCAGGCCAGAAGGAACAGAGCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGGCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGGAGTTGACCCCGTTAGCCTGGACCCAC
 GTGGCCTCCAGGAGGCACTCAGTGCCCGATCCCCCTCCAGAGGGCTCTGCCAGGGTGC
 CACCCACTGTGTCAGCAGCACCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
 TTTCCATGATGAGGCCTGGTCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGGCCTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACACTCAAG
 TCTGCTCTAGCGAATATGTGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCGGATGCTGGGGCCACCAGGCCACCGGGATGTGCTGTCT
 TCATGGATGCCACTGCGAGTGCCACCCAGGCTGGCTGGAGGCCCTCCTCAGCAGAAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTATAGATGTGATTGACTGGAAGACTTCCAGTA
 TTACCCCTCAAAGGACCTGCAAGCGTGGGTGTTGGACTGGAAGCTGGATTCCACTGGGAAC
 CTTGCCAGAGCATGTGAGGAAGGCCCTCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGGTGGTGGCCATGGACAGACATTACTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTCGCTGCAAGGTGGTAAAACCTCGAACTGTCTTCAAGGCCTGGCTCTGGT
 GCTCTGTTGAAATCCTCCCTGCTCTGGTAGGACACATCTACCAAAATCAGGATTCCCAT
 TCCCCCCTCGACCAGGAGGCCACCTGAGGAACAGGGTTCGATTGCTGAGACCTGGCTGG
 GTCATTCAAAGAACCTTCTACAAGCATAGCCCAGAGGCCCTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTGCAAGCAGACTGGGTGTCGGACATTCACTGG
 TTTCTGGCTAATGTCTACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTCTCTGGAAA
 GCTCCACAACACTGGACTTGGCTCTGTGCAGACTGCCAGGAGAAGGGGACATCCTGGGCT
 GTCCCATGGTGGCTCCCTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
 AGGAAGGAGATTCACTTGGCAGGCCACAGCACCTGTGCTTGCTGTCAGGCAGGAGCAGGT
 GATTCTCAGAACTGCACGGAGGAAGGCCATCCACCGAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATTCTTCTGGGAAATGCATGGAAGCTGTGGTGAAGAAAAC
 AATAAAGATTGTACCTGCGTCCGTGTGATGGAAAAGCCGCCAGCAGTGGCGATTGACCA
 GATAAATGCTGTGGATGAACGA**TGA**ATGTCAATGTCAGAAGGAAAAGAGAAATTGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTGAGAAGCTGATCCTTGTGT
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTATGAAAGAATATAGGAAGTTCTCCTT
 TCACACCTTATTCATTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFWEPLPEHVRKALQSPISPPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIFYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEPDCMERLQLQRLGCRTFWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQLVQNCTEEGLAIHQHQHWDFOENGIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGAC**ATGGA**
 GTCCAGGATGTGGCCTGCGCTGCTGCTCCCACCTCCTCCCTCTGGCCACTGCTGTTGC
 TGCCCCCTCCCACCGCCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCCACCAGCCCCAGCC
 CGCCCCCCCCTGTGCCAGGGGAGGCCCTCGGCCCCACGTCACTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCAAGATCACGTCGGCAAGTCTGCCTGGCACTG
 CACCCCCAGCCACCCCATCAGGCTTGAGGAGGGGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGTCCCACCGTGTCTCGAGAGGATGGAGGGACCCAACTCTGCCAATCCCGG
 ATTCTGGACTATGGTTTGAGGCCCTCATGGGCTCGAACCCACACCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTGGAGAGGCACCTGCCACCTGCCGCCCCATT
 CTGTTGGGGGCCGTGGGAAGGTGTGGACCCCCAGCTCTATGTACAATTACCATCTCCAT
 CATCATTGTTCTCGTGGCACTGGCATCATCTCAAGTCTGCTGGACCCAGCCAGAAGC
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGAGGGAGAGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCAGTGTGCTGGGGCCTCGGGGACTCACCTACCCCCACCC
 TGACCATGAGGAGCCCCGAGGGGACCCCGCTGGATGCCAACCCAAAGGGGCTCCAG
 CCTTCCAGTTGAACCGG**TGA**GGGCAGGGCAATGGGATGGGAGGGCAAAGAGGGAAAGGAAAC
 TTAGGTCTTCAGAGCTGGGTGGGGTGCCTCTGGATGGTAGTGAGGAGGCAGGCGTGGC
 CTCCCACAGCCCTGGCCCTCCAAGGGGCTGGACCAGCTCCTCTGGGAGGCACCCCTTC
 CTTCTCCCAGTCTCTCAGGATCTGTGCTATTCTGCTGCCATAACTCCAACCTGCCCC
 TCTTGTTTTCTCATGCCACCTGTCTAAGACAACCTGCCCCCTTAACCTGATTCCC
 CCTCTTGCTTGAACCTCCCTCTATTCTGGCCTACCCCTGGTTCTGACTGTGCCCTT
 TCCCTCTCCTCTCAGGATTCCCTGGTGAATCTGTGATGCCCAATGTGGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGCCACAGCCCCATCCCAGTGGGTGGGGCAGCTGTGGGG
 GCTGGGGCCACAGGGCTCCTGGCTCTGCCCTTGACACACCACCCGGAAACACTCCCCAGCC
 CCACGGCAATCCTATCTGCTGCCCTCCTGCAGGTGGGGCCTCACATATCTGACTTCG
 GGTCCCTGTCCCCACCCCTGTGCACTCACATGAAAGCCTGCAACTCACCTCACCTC
 AGGCCATTGACACGCTCTGCACCCCTCTCCCAGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCGTCTCACATTGCACTCTCTCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTCTGCACACTTACCTCTCATGTGCGTTCCGGCCTGATGTTGGTGG
 TGTGCGGCGTGTCACTCTCCCTCATGAACACCCACCCACTCGTTCCGCAGCCCTGC
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGCTCCTGGGCCCTCATGGTCATGG
 TCTCGTCCCATTCCACACCATTGTTCTGTCTGCTCTCCCATCCTACTCCAAGGATGCCGG
 TCACCCCTGAGGGCTCCCCCTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGGCC
 CTGCTAAAATCTGTTCTGACAGATGGGTTGGGGAGTCGCCTGCACTACATGAGAA
 AGGGACTCCCATTGCCCTTCTCCTACAGTCCCTTTGTTCTGCTCTGCTGCCCTGGCT
 TCTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTCCAGCCT
 CCCCTGGGCCTCCCTAACCTCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC
 ATCGGGAGCTGCTCCACAGTCTACCCCTCCGGACTCCCTGCTGCCCTCAGGTT
 CCTCCCTCCTCTCACTGGTTTCCACCTCCTCCCTTCTGCTCTGCCCTTCCCTGGCTC
 GTGATATATATTTGTATTATCTCTTCTTGTGGTGTGATCATCTGAATTACTGTG
 GGATGTAAGTTCAAAATTCAAATAAGCCTTGCAAGATAA

FIGURE 204

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAA SPQR LRGLLL LQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMR SNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAI IYLDQGSPEMN
STINI HRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKG DASTGWNSVSRIII EELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCGAGCGCAGTCCTCCGTGCGTCCC GCCGCTGCCCTCACTCCCGGCAGG**ATGG**
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGGTCTCCGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCGTGCCACGCTGTGGAACGAGCCGGCGAGCTGCC
GTCGGGAGAAGGCCCGTGGAGAGCACCAGCCCCGGCCGGAGCCGTGGACACCGGTCCCC
CAGCCCCCACC GTCGCGCCAGGACCCGAGGA CAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGCCCGCGCTATCGCGGCCATCGT GATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGCTGAGAAAGTTCTGCCTCC**TGA**AGCGAATAAA
GGGGCCGCGCCGGCCGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 206

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristylation site.

amino acids 91-96

FIGURE 207

GGCGTGGTGGTGGCGCGGCTGAAGGGTGTGGCGAGCAGCGTCGGTGGCGGG
 CGGGCCGGGACGGGCA**AT**GGCCCTGCTGTGCCTGGTGTGCCTGACGGCGCGCTGGCCA
 CGGCTGTCTGCACGCCAGCAACTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
 ACTTCAAGTCCTGGTGGGTGGCGACATCCCCGTGTCAGGGCGCTGCTACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAAGATGATGGATCAGCTGTACCAAGGGAAAGATGTACTTCC
 CCGGGTATTCCCCAACGAGCTGCAGAACATCTTCCGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGAGGAGGGCAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATACCCCCGGGGACCTCCCC**TAA**GTAGCCC
 CCAGAGGCGCTGGAGTGTGCCACCGCCCTCCCTGAAGTTGCTCCATCTCACGCTGGGG
 GTCAACCTGGGACCCCTCCCTCCGGGCATGGACACACATACTGAAAACCAGGCCGCAT
 CGACTGTCAGCACCGCTGTGGCATCTCCAGTACGAGACCATCTCTGCAACAACTGCACAG
 ACTCGCACGTCGCCTGCTTGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
 GCCAGGGCCCTACTGTCCCTGGGTCCAGGCTCTCCTGGAGGGGCTCCCGCCTCCAC
 CTGGCTGTATCGGGTAGGGCGGGCGTGGGTCAAGGGCGCACCCTCCAAGCCTGTGT
 CCCACAGGTCTCGCGCAGTGAAGTCAGCTGTCCAGGGCCTCTGAACATACATAAAAC
 TGGCACAAGTAAGTCCCCTCTCAAACCAACACAGGCAGTGTGTATGTGAGCACCTCGT
 GGTGAGTATGTGTGGGCACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGCTCCGA
 GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCAGCTGCAGTCCTTCTCCCTCAAAG
 GTCTCCGACCCTCAGCTGGAGGCAGCTTCAGACAGGACACGAGCATGAGGTAAGGCCGC
 ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGAGGGTCCCTACGATGGTTAGGGTGCCTCC
 ATGGAGGGCTGACTGCCACATTGCCCTTCAGACAGGACACGAGCATGAGGTAAGGCCGC
 CCTGACCTGGACTTCAGGGGAGGGGTAAAGGGAGAGAGGAGGGGGCTAGGGGGCTCC
 AGATCAGTGGGGCACTGCAGGTGGGCTCCCTACCTGGACACCTGCTGGATGTCAC
 CTCTGCAACCACACCCATGTGGTGGTTCATGAACAGACACCAGCTCTGCCTCTGG
 CCTGGACACACAGAGCCACCCGGCCTGTGAGTGACCCAGAGAAGGGAGGCCTGGGAGA
 AGGGGTGCTCGTAAGCCAACACCAGCGTGCAGCCCTGCACACCCCTGGACATCCAGGC
 ACGAGGGTGTGAGTGTGGCACACATAGGACCAACACGTCCCAGCTGGAGGGAGAGGCCT
 GGGGCCCCAGGGAGGGAGGCAGGGGTGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
 TGGAAAGATGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGCCTGCCAGGGCAAC
 GTGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACCTGGAGCTGGCTGCTGCTGC
 CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCAGGAGGGGGAGG
 GAGGGAATGGGGTGGCTGTGCGCAGCATCAGCGCCTGGCAGGTCCGAGAGCTGCGGG
 TGTGATTAAAGTCCTGATTTCTC

FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI
PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMMDQLYQGKMYFPGYFPNELRN
IFREQVHLIQNAAIER
HLAPGSWGGQLSREGPSLAPEGSMPSPRGDLP
```

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCGTCCAGGTTCATGTTCCCTTTATTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGCCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTCCAGGATTAGAAATACCAGCAGTGCCACTCCA
 TAGCATGGTGCAAAAATTCCCAGGCAGTCATTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGAACACCATCTGCCTCTTCGCCTGGTAGACAATGAACAACTG
 AATTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGACTGTGATTGGTTATTCAACAGCG
 TAATTCAAGATTCATCTCCTCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTCCAGGGAAAGATTCTCTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTCAAACTAAAGGAGTCTCAACTGCCAG
 CTTGGCAATTACCAAGACTCTAGATGACGAGTGGATACACTGCCACAGCAGAAGTTCC
 GTAGAGCATGTGCAAAACTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**TGA**CTTCTCCTGGAACTACATATGCC
 AAGTATCTACTTATGCAAAGTAAAAGGCACAACCAAATCTCAGAGACACTAAACAAACAG
 GATCACTAGGCCTGCCAACACACACACACACAGCTCATTCCCTGTCTAAATCTCGTTCTC
 TTCTCCTCTTTAAATTTCATATCCTCACTCCCTATCCAATTCCCTTATCGTGCATT
 CATACTCTGTAAGCCCACATGTAACACACACTAGATCAAGGCTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCAATTGTCATTAATATCAAGT
 TTGTATACTGCACATGACTTACACACACATAGTTCTGCTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTCTTCTAAGCACATGTCGTCTGACTCAGGATCAAAACCAAAGG
 ATGGTTTAAACACCTTGTGAAATTGTCTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTGGTTAGCATCTCCAACCTCC
 TATGTAATCAACAACCTGCATAATAAATAAAAGGCAATCATGTTATA

FIGURE 210

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLLFLLTCELAAEVAEEVEKSSDGPAAQEPWTLDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRLVVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTIVIGLFNSVIQIHLLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDGMKENGKVISFFKLKESQLPALAIYQTLDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGGCTGGGACCGGAGTGGGGAGCGCGGCCTGGAGGTGCCACCCGGCGGGGTG
 GCGGAGAGATCAGAACCTCTCCCCAAGCCAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGCGGGCGGCGACTGCAGTGGCTGGAC**GATG**GCAGCGTCCGCCGGAGCCGGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTCTGGCGGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTGGAAGTATACGCCAAAAGAAATCTCGTGGCAA
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCTGGAGCTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTCCACTACTC
 CCAAGGGCAAGTGTACCTGGATTATCCACCATTAAAGACAGAACATCAGCTGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCACATAGAAAATATGCAGTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCAGCCTGGACACATTAGGCTCTA
 TGTCGTAGAAAAAGAGAATTGCTGTGTTCCAGTTGGTAGTGGTGGCATAGTTACTG
 CTGTGGCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAA
 AACTCTAACGGATTACACTGGCTGCAGTACATCAGAGAGTTGTCACCAGTTAACGAGGC
 TCCTCGGAAGTCCCCCTCGACACTGAGGGCTTGTAAAGAGTCTGCCTCTGGATCTCACC
 AGGGCCCAGTCATATATGCACAGTTAGACCACCTCCGGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGGGTATGCGGATATCGAAAGAAT**TAA**GAGAACATACCTAGAACATATC
 CTCAGCAAGAACAAAACAAACTGGACTCTCGTGCAGAAATGTAGCCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
 ACAAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTGCATGA
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGCTGTTTGTACTTCTTTTC
 AGGTCATTACAATTGGGAGATTCAGAAACATTCTTACCATCATTAGAAATGGTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTCCAGTAGACATGGCCTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTACAGTACGTTAGTACGTTAGTGGCTGCCGCTTTAAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTGAGAAGTTTTGAAGTTTCTCACT
 AAAATATGGGCAATTGTTAGCCTTACATGTTGTAGACTTACTTAAGTTGCACCCCTG
 AAATGTGTATCAATTCTGGATTCTACAGTACGTTAGTAAAGTAAAGCTTCAAGCTTGCCTT
 GTCACCTCATTCTGGACACAGTTGGATCAACTGATGATGAGTAAAGTAAAGCTTCAAGCTTGCCTT
 GAGAACTTTGTAAACGTGGAGAGTAAAAAGTATCGGTTTA

FIGURE 212

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVLYGNYPFFKDRISWAGDLDKKDASINEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSINKSESVVYADIRKN
```

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGACTGCCGGCTGCCGCC
 CCCGGGGCTTGGCCTCAAGCTGCGGACGACGCCGGTCCATCAGCGCGCCGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGGGGCCTCGGGCTGGGGCTGGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGCGCGGCCCGGCAGTCCCCCGCGGCCCGACCCTGAGGCG
 TCGCCTCTGGCGAGCGCCACAGGAGCAGTCCTCGCCCCGTGGTCTCCGCAGACCCC
 GCCGCCCTGCTCCAGGTGCTCGCCAGGCCATCGAGAGCAGCCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGCGCACCGGCATAGTGGTTGGAGTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTGCCAAATTGTGGAAAG
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTCTGTACAACAAGATTACTGATTCCCATTAAAGTGGATT
 TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTGAAGATGA
 TGAAAGAGAATGTTGCATTGAGCAAGAAAAGAAGGCAAAAGTAATGAAAAGAATGATT
 ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAATGCCGAATTCAAACCTGGCAAGAA
 AAAGAATGATTGAAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATTCAATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTGTCTCAAAACCTGGTAGTCAGTTTGATTCA
 ACTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTCAGGATGTAAATATTGGA
 CTATATGCAGAAAATTCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAACGAGC
 CAGTGATTACAATAGAGCAAGG**TAA**ATGAATACTTCTGCTGTCTAGCTATATCGCATC
 TTAACACTATTTATTAATTAAAAGTCAAATTCTTGTCTTCCATTCAAAATCAACCTGC
 CACATTGGGAGCTTCTACATGTCTGTTCTCATGTAAAGTGAAGGAAGTAAAACA
 TGTTTATAAAGTAAAAAAA

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPPDPEASPLAEPPEQSLAPWSPQT PAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSITMVALAKLWEAGKLDD
IPVQHYVPEFPEKEYEGERVSVTLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPMVYNRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACCGTACGTAAGCTCGGAATTGGCTCG
AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGTGGGCAACCCGGCTGCTCCTGC
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCAGGGCAGCGGCTGCCGGCCGGACT
GGTGCAGGAGGGCTGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGCTGCT
GCTGGAGCACTCATTGAGATCGATGACAGTGCAACTCCGGAAAGCAGGGCTCACTGCTCT
GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
CGACTCCGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCAAGGCGACCCGG
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTGTCCCTGCGTGCTCCCTGG
TGGAGTCGACCTGTCGGACCAGCTGACCTGCACGTGGATGTGCCGGAACGTGGTGGG
GTGTCGGTGGTGACGCACCCGGGGCTGCCGGGCATGAGGTGGAGGACGTGGACCTGGA
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCG
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
TCCTTCTCGCAAATACTGGATGTACATCATTCCGTCGTCTGTTCTCATGATGTCAGG
AGGCCAGACACCGGGGCCAGGGTGGGGTGGGGTGGTGGTAGTGGC
TTTGTGTGTGCCACCCCTCCCTGTAAGTCTATTAAAAACATCGACGATACTGAAATGTG
TGAACGTTTGAAGCTACAGCTCCAGCAGCCAAAGCAACTGTTGTTGGCAAGACGG
TCCTGATGTACAAGCTTGATTGAAATTCACTGCTCACTGATACTGTTATTCA
GAATGGCTGTCCCCATCCTCATGTGGCTGTGGAGCTCAGCTGTGTTGTGGCAGTTAT
TAAACTGTCCCCAGATCGACACGCAAAAAAAA

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pi: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPSRARGSGCRAVTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLWNQQDGTLSLSQRQLSEEERGRRLDVAALNGLYRVRIPRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQAKNPQEOKSFFAKYWMYIIPVVLFLMMMSGAPDTGGQ
GGGGGGGGGGSGLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCGAGCCGGAGCCGGAGCCACAGCAGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCCCGCAGACCGGGGCAGCAGGTGTCGTCGGGGGCCACC
ATGCTGGTGACTGCCTACCTGCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGCTGGAACCT
 GTCAAGATGCCGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATGCCATCCTCATGTCTG
 TGGCCTGCCTCTACAGTCCTTTGGCCTAGTGGCCTCCTCCCTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGTCCTCTCCCTGACTTAACCAAACTCTCT
 CAAGACTACTTGTGCTGCTAGTGGGGCAGCACCTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCTGCTGAGT
 GGATCCCAGCTACCTTGCTCGAGCTGCCTTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGCCTGTAGGCCCTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGCCTTGGCCCTCGAAACTGGGGGAGAACTATGACC
 GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGCGACCGCCGC
 GTGCTGCTGCTGGCACCATAAGCTCTATTGAGAGTGTCACTTCATCTTGCTTCCCT
 CTGGACACCTGTGCTGGACCCACACGGGCCCCCTGGCATTATCTTCTCCAGCTCATGG
 CAGCCAGCCTGCTGGCTTCCCTGTACCGTATGCCACCTCCAAGAGGTACCACCTCAG
 CCCATGCACCTGCTGTCCCTGCTGTGCTCATCGTCGCTCTCTCTTGTACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTCATAGCCTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTCCCAGCATGAGCTTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTCCGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
 CCTTGTCCCTCATGACAGTGATCGAAAAACAGGCACTCGAATATGTTCAGCATTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGACTCTTCACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTCACCTACTGAGGAGGCCATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGACAGACTCTGAATTCCAGCTATCCGGGATTGTACAGATCTCTGT
 GACTGACTTTGTGACTGTCCGTGGTTCTCCCTGCCATTGCTTGTGTTGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAGTCCCTCTGTTACTCCCATTAGAAA
 ATAAACACTTTAAATGATCAAAAAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIIFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPE
EQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAVVGLFTVVRHDA
ELRVPSPTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGGCGGGCGAGAGGAAACGCGGCCGGCCGGCCCTGGAG**ATG**
GTCCCCGGCGCCGGGCTGGTGTCTCGTGTCTGGCTCCCCGCGTCGTCGCGGCCA
CGGCTTCCGTATCCATGATTATTTGTACTTCAAGTGCTGAGTCCTGGGACATTGATA
TCTTCACAGGCCACACCTGCCAAGGACTTGGTGGTATCTTCACACAAGGTATGAGCAGATT
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGAACTCAGCAACGGTTCTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTGACAACGCAGTGACAATGACAGCTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTCCCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTGGAACAGCATGGCTGCCATGGGCCATCATT
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGGTAGAAGAGTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGAAACCC
AGGAATTGGTACTTGGAAATTGGAGATAGCATCTGGGACAAGTGGAGGCCAGGTAGAGGA
AAAGGGTTGGCGTTGCTAGGCTGAAAGGAAGCCACACCACTGGCCTCCCTCCCCAGG
GCCCCAAGGGTGTCTCATGCTACAAGAACAGGGCAAGAGACAGGCCAGGGCTCTGGCTA
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
CACCTGGCTCCAGCCTCCCCACCCAGGGTCTGACAGTGACCTCACAGCAGTTGG
AGTGGTTAAAGAGCTGGTGTGGACTCAATAAACCCCTACTGACTTTAGCAATAAA
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAA

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWL PACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATC**ATG**GAACTTGCACTGCTGTGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCAGTCGGACTAGGTGGCAG
AGGCCAACCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACTTGTATGGAT
TTATCTCAACGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC
CGAA**TAA**AAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFNVIYLENEDSE
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTCCTCTGGATGGGGGCCAGGGGCCAGGAGAGTATAAAGGCATGTGGAG
GGTCCCCGGCACACCAGACGCCAGTCACAGGCAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTGCCCTCCTGGGGGCCACCTGGCAGGGAAAGATGTAT
GCCCTGGAGGAGGCAAGTATTTCAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTCCTGGTAAAAAGTGTCCAGGTGAAACTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTAGGTGGAAATACCCAGGAAGTCACCCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTGTGCCTCCAAGCTTCCTCCGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTCTATTTGGGAAGCTTGATGCCAGATCTCCTGCCTACCCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGCCAGTATCAACTCCTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACTCACCGTGGTCGC**TAG**GGTGGGTATGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAAGTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLKVSVQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCCTCTGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATCACGGAACTGCTGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCCTGGAAGAATACATCATGTTTCGATAAGAAGAAATTGTAGGATCCAGTT
 TTTTTTTAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAGATGCAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTGATGTTGCTGCGAATGCGGTGTTGGGATT
 TATTGTTCTGGAGTGTCTGCGTGGCTGCAAAGAATAATGTCAAAATCGGCCATCT
 CCCAAGGGGTCCAATTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGCTGTCATGCAACTGGCCCTAAGCAAAGCAGCTAAGGACGACCTTGAA
 CAATACAAAGG**A**TGGGTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTTAUTGACAATGCTTCTGCCAACGAGGATGCCCTAACGGCTG
 TAGGTGTGAAGGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTGTCCTCGCTATAACAGCCTCAAAACTTAAGTATAAT
 CAATTAAAGGGCTAACCAGCTCACCTGGCTATACCTGACCATAACCATATCAGCAATAT
 TGACGAAATGCTTTAATGGAATACGCAACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTCTAACATACCTTCAGACCTGTGACAAATTACGGAACCTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGATCTGAACAGTTCGGGCTTGCGGAAGCTGCTGAGTT
 ACATTACGGCTAACCTCCCTGAGAACCATCCCTGTGCAATATTCCAAGACTGCCGCAACC
 TGGAACTTTGGACCTGGGATATAACCGGATCCGAAGTTAGCCAGGAATGTCTTGCTGGC
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTCAGCTCAACCTGGCCCT
 TTTCCAAGGTTGGTCAGCCTCAGAACCTTACTGCACTGGAAATAAAACTCAGTGTCAAG
 GACAGACCATGTCCTGGACCTGGAGCTCCTAACAAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCAGCTGCAACCTGGAA
 TTCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACA
 TCAGTCTGCTGGGAATATGGGAATGCAGCAGAAATATTGCTCCCTGTAAACTGGCTG
 AAAAGTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT
 TTGATCTGCCAGGGCTCTCCAAAGCCGACGTTAACCCAGCTCCAGGCCAGAGACCGATGC
 GAGAGCAAACCCCTTGCCCCCGACGGTGGGAGCCACAGAGCCGCCAGAGACCGATGC
 TGACGCCGAGCACATCTTCCATAAAATCATCGCAGGAGCTGGCTTTCTGTCC
 TGCTCGTCATCCTGCTGGTTATCTACGTGTATGGAAGCGGTACCCCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATCGAAGGCACAGGAAAAGAAAAGACAGTCCCTAAAGCAAAT
 GACTCCCAGCACCCAGGAATTATGTGAGATTAAACCCACCAACACGGAGACCAGCGAGA
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTAAAGCTGGAAATAAGTGGTGCTTATTGAAC
 TGTTGACTATCAAGGGAACCGCATGCCCTCCCTCCCTCCCTCACTTGGTGG
 CAAAGATCCTCCTGTCCGTTAGTGCATTATAACTGGTCATTTCCTCTCATAACATA
 ATCAACCCATTGAAATTAAATACCAATCAATGTGAAGCTGAACTCCGGTTAATATAA
 TACCTATTGTATAAGACCCTTACTGATTCCATTAAATGTCGCAATTGTTAAGATAAAACT
 TCTTCATAGGTAAAAAAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTVLLTMSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTLRNLDLSYNQLHSLGSEQFRGLRKLLSLHRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNLAFFPRLVSLQNLQWNKISVIGQTM
SWTWSSLQRDLDSGNEIEAFSGPSVFQCVPNLQRLNLDSNKLFIGQEILDWSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELOGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPSTQE FYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAACCCTATCCTAAGTTGACTGTCCTT
TAAATATGTCAGATCCAGACTTTCACTGTCACCTCAGCGATCTCACGATAGGGATCTTG
TGTTGCCGCTATTCCAGTTGGTCTCGGACCTACCAGCGAAGAAGATGAAATGTGTGT
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGGTTTGG
TGGCAGCTCTCTGTGGAGCTGTGGCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCGA
ATTGATTCTCACAGGCGCACCATGGCAGTTTGCTGTTGGAGACTGGACTCTATTATGG
GACAGAAGCAGCTGTGAGTCCAACCTGGGAATTCACCTCAAACACTAAACCCCTGACCTAT
ATCCTGTTCCATGCTCCATGTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
AAAACAACTGATTTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCA
AACATCAAATTAGGAATAGTTATTCACTGTTGGAAATGTCCAGAGATCTATTCAATA
GTCTGAGGAAGGACAATTGACAAAAGAATGGATGTTGGAAAAATTGGTCAATGGAGATG
TTTAAATAGTAAAGTAGCAGGCTTGATGTGTCAGTGCTGTATCATACTTTATGCTACAC
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
TCCATCACATTAGGACTCCACTGCAGTATACAGCACACCATTCTGCTTAAACTCTTC
CTAGCATGGGTCCATAAAATTATTATAATTAAACAATAGCCCAAGCCGAGAATCCAACAT
GTCCAGAACCAAGAACCAAGAAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
GAAAAGTTGGAGTTGAAGGGTAAAGGATAATGAAGAGGAAAGGAAAGATTACAAGTCT
CAGCAAAACAAGAGGTTTATGCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGAGAAAAGAAAATTCCC
CTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
GCATTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCATGAGGACTGC
AGAAGTAGCAATGAGACATCTCAAGTGGCATTGGCAGTGGCCATCAGCAGGGGACAGA
CAAAACATCCATCACAGATGACATATGATCTCAGCTGACAAATTGTTGAACAAACAAAT
AAACATCAATAGATATCTAAAAA

FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMCVNNDQHPNGWYIWILLLVLA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAGDLDIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGC GGAG TAAATCTCCACAAGCTGGGAACAAACCTCGTCCC ACTCCCACCCACC GGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTCGCCAGTGTGGACGCAGCTGACGCCCGCTTATT
 GCTCTCGCTCGTCGCCCGCTCAGAAGCTCCGTGGCGCGACCGTGACGAGAACCCC
 ACGGCCAGCTCAGTCTCTTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTAAACT
 CCCTCTCAAAACTCATCTCCGGGTGACTGAGTTAATAGAGTGGATAACACCTGCTGAAG
 ATGAAGAATATAACATATTGAGGATATTTTTCTTTCAAGTCTGATTGTGGC
 TTACCTCAAGTTACCATTTCAAGTCAGTCTGTTGTTGCTTCAAGAA**ATG**TTTTTA
 CAATCTCAAGAAAAAAATATGCCCCAGAAATTGAGTTACTGTTGCTGTATTGGACTCATT
 TGGGGATTGATGTTACTGCACTATACTTTCAACAAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCCTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATT
 GCTGTCCTCTGGATGACATTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGGTGTGAATGGCTCAGCAGCCAACACCAATGGTACTAGTGGAAATTGGTGCCAGTAA
 CCACAAATAAAAGAACGAATGTCGGGCAGTATCAGA**TAG**CAGTTGAAAATCACCTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTATAATTGCTGGCTTAGGAC
 AGAGCAAAACTTACAATAAAAGCTCTACACATTCAAGGAGTATGCTGGATTGAAAC
 TCTAATTCTGTACATAAAATTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATG
 CTGTAATGTCCTAAAGAGAATTGGTAACTGGTGATGGTAAGCAGATAGGTGAGT
 TTTGTATAATCTTTGTGTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTC
 ATTCTATAACACATTATTAAAGTATATAACACGTTTTGGACAAGTGAAGAATGTTAA
 TCATTCTGTCATTGTTCTCAATAGATGTAACTGTTAGACTACGGCTATTGAAAAATGTG
 CTTATTGTAATATTGTTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAA
 TAATGTTGAAATCATGACCCAAAGAATGTATTGATTGACTATCCTCAGAATAACTGA
 AGGTTAATTATTGTATATTAAAAATTACACTTATAAGAGTATAATCTGAAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGCAATTAAATAACAGCATTAAAGTT
 GTAAACTCTAATCTTAACTTATTGAAGAATAAAAGATATTGATGAGAGTAACAATA
 AAGTATTGATTGATTGTTACATACATGAATGTCATTAAAGTTAATCCTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTTCATATTCCATATTGGGTAATTGCTTTATTATATTGGTC
 TAGGAGGAAGGGACTTGGAGAATGGAACCTTGAGGACTTAGCCAGGTGTATAATAAAA
 GGTACTTTGTGCTGCATTAAATTGCTGGAAAGTGTAAACATTATATTATAAGAGTATC
 CTTATGAAATTGAAATTGTATAACAGATGCATTAGATATTCAATTATATAATGGCCAC
 TTAAGAACATTAAACTATGAAGATTGACTATCTTTCAGGAAAAAGCT
 GTATATAGCACAGGAAACCTAATCTGGGTAATTCTAGTATAAAACAAATTATACTTTAT
 TTAATTTCCCTGTAGCAAATCTAATTGCCACATGGTGCCTATATTCAAGTATTATT
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTCTAGATTAGACTATATAAGAATTAGATAT
 TGTATTGTGTCATTATAATATGCTACCATGAGCAATAATTACAATATTGTTATTAAAA
 TAAATATGTGAAATATTGTTCATGAAAGACAGATTCCAATCTCTCTCTGT
 CTGTCTACCTTATGTGAAGAAATTAAATTATGCCATTGCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 231

CGCGGCCGGGCGCCGGGTGAGCGTCCGAGGCCTGTCGGCGCAGGCTCCAGCCCCAC
CATGCCGTGGCCCCTGCTGCTGCTGGCGTGAGTGGGCCAGACAACCGGCCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTCGACAGCTCAGCCTGACTCGG
 GTGGATTGTAGCGGCCCTGGGCCCCACATCATGCCGTGCCATCCCTCTGGACACAGCCA
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGCT
 ACACGACGTGGCTGGCCTGGATCTCAGCCACAACTGCTCACCAAGCATCTCACCCACTGCC
 TTCTCCCGCCTTCGCTACCTGGAGTCGCTGACCTCAGCCACAAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTTCACCAGCTCACCCCTGAGCGACGTGAACCTAGCCACAAACCAGCTCCGGG
 AGGTCTCAGTGTCTGCCTTCAGCACAGTCAGGGCCGGCACTACACGTGGACCTCTCC
 CACAACCTCATTCACCGCCTCGTCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCACCAT
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGC
 TGGCCTACCTGAGCCTGGATGGAACCCCTAGCTGTATTGGTCCGGTGCCTTCGCGGGG
 CTGGGAGGCCTTACACACCTGCTCTGCCAGGCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTTCCGTGAGTACCGGGCCTGCAGGTCTGGACCTGTCGGCAACCCAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTCAGGCCTGAGCTCCCTGAGGAGCTGGACCTTCGGGACCC
 AACCTGGTCCCCCTGCCTGAGGCCTGCTCCTCACCTCCGGCACTGCAGAGCGTCAGCGT
 GGGCCAGGATGTGGGTGCCGGCGCCTGGTGCAGGGCACCTACCCCCGGAGGCCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGAATCTGCTGCCAGGGGGCCACC
 ATCTG**TGA**CAAATGGTGTGGCCAGGGCACATAACAGACTGCTGTCTGGCTGCCTCAG
 GTCCCGAGTAACTTATGTTCAATGTGCCAACACCAAGTGGGAGGCCAGGCCTATGTGGCA
 GCGTCACCACAGGAGTTGTGGCCTAGGAGAGGCTTGGACCTGGGAGCCACACCTAGGAGC
 AAAAGTCTCACCCCTTGTCTACGTTGCTTCCCCAACCATGAGCAGAGGGACTTCGATGCCA
 AACCAGACTCGGGTCCCCCTCTGCTTCCCTCCCCACTATCCCCAACGTGCCTTCCCTCAT
 GCCTGGGCCGGCCTGACCCGCAATGGCAGAGGGTGGTGGGACCCCTGCTGCAGGGCAGA
 GTTCAGGTCCACTGGCCTGAGTGTCCCCTGGGCCATGGCCAGTCACTCAGGGCGAGTT
 TCTTTCTAACATAGCCCTTCTTGCCATGAGGCCATGAGGCCGCTTCATCCTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAAATCAAGTCCACCCCTCTCATGTGAC
 AGATGGGAAACTGAGGCCTGAGAAGGAAAAGGCTAATCTAAGTTCCTGCGGGAGTGGC
 ATGACTGGAGCACAGCCTCTGCCTCCCAGCCGGACCAATGCACTTCTGTCTCCTCTA
 ATAAGCCCCACCCCTCCCCGCCTGGCTCCCTGCTGCCCTGTTCCCCATTAGCACA
 GGAGTAGCAGCAGCAGGACAGGCAGAGGCCTACAAGTGGACTCTGGCCTCTGACCAGCT
 GTGCGGCATGGCTAAGTCACTCTGCCCTCGGAGCCTTGGAGCTAGGGCACATTGGTT
 CCAGCCTAGCCAGTTCTCACCCCTGGTTGGGCCCCAGCATCCAGACTGAAACCTACC
 CATTTCCTCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
 TCTGGCTGGATCTCAAGGGCCTCTGGATTCAGTCCCCACTGGCCTGAGCACGACAGC
 CCTTCTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC
 TCTACCCCAAGGGCAGCATTCTCAGCTTCCGAACCCCTGGCTGTTCTTAGTCTTCTATT
 TAAAAGTTGTTGCCCTTTAACGGAGTGTCACTTCAACCGGCCCTCCCTACCCCTGCTGGC
 CGGGGATGGAGACATGTCATTGTAAGCAGAAAAAGGTTGCATTGTTCACTTTGTAAT
 ATTGTCCTGGGCCTGTGTTGGGGTGTGGGGGAAGCTGGCATCAGTGGCACATGGGCATC
 AGGGGCTGGCCCCACAGAGACCCCACAGGGCAGTGAAGCTGTCTCCCCCACCTGCCTAGC
 CCATCATCTAACCAGGTCTTGATTTAATAAACACTATAAAAGTTAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRLRYLESIDLDSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDSLHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRPELAPS
GFRELPGHQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSPPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCGATTCTCCCCAGTTCCCCTGTGGGTCTGAGG
GGACCAAGGGTGAGCTACGTTGGCTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATTCCCCA
AAACAAGTTTGACATTTCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCT
GTTCCAGGCCTTACCTGCTGGGACTAACGGCGGAGCCAGGATGGGACAGAATAAAGGAGC
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTCTTCAC
GGGAGGCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTCAAGGCTAAGATGAAAGCC
TCTAGTCTTGCCTTCAGCCTCTCTGCTGCCAGTTATCTCCTATGGACTCCTCCACTGG
ACTGAAGACACTCAATTGGGAAGCTGTGTGATGCCACAAACCTCAGGAAATACGAAATG
GATTTCTGAGATACGGGGCAGTGTGCAAGCCAAGATGGAAACATTGACATCAGAATCTTA
AGGAGGACTGAGTC TTGCAAGACACAAAGCCTGCAATCGATGCTGCCTCTGCCATT
GCTAAGACTCTATCTGGACAGGGTATTAAAAACTACCAGACCCCTGACCATTATACTCTCC
GGAAGATCAGCAGCCTGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCAT
GCCCATGACATGCCATTGTGGGAGGAAGCAATGAAGAAATACGCCAGATTCTGAGTCA
CTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTGGGGAACTAGACATTCTC
TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT
CAAGAGCTCCAGTCTCAATACCTGCAAGAGGGCATGCCAAACCAACCATCTCTTACT
GTACTAGTCTTGTGCTGGTACAGTGTATCTTATTCATTGCTTGCATTGCTTCCTGCATGAT
TGTCTTATGCATCCCCAATCTTAATTGAGACCATACTGTATAAGATTTGTAATATCTT
TCTGCTATTGGATATATTATTAGTTAATATATTATTATTGCTATTAAATGTATT
ATTTTTTACTGGACATGAAACTTAAAAAAATTCAAGATTATTTATAACCTGACTAG
AGCAGGTGATGTATTTATACAGTAAAAAAAAACCTGTAATTCTAGAAGAGTGGCT
AGGGGGGTATTCAACTAAGGACATATTACTCATGCTGATGCTGTGAGA
TATTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTGATGTGGAATT
GCACATCTACCTTACAATTACTGACCACCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAAGTTTCTTCATA
CCAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTILNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLRHLLRLYLDdrvFKNYQTP
DHYTLRKISSLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTCGCGCTACTGCTGAATGTCCGTCCCAGAGGAGGAGAGGCTTTGCCG
CTGACCCAGAGATGCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGCGCTACCGTGGC
CGAGCTAGCAACCTTCCCCTGGATCTCACAAAAACTCGACTCCAAATGCAAGGAGAAGCAG
CTCTTGCTCGGTTGGAGACGGTGCAAGAGAATCTGCCCTATAAGGGAATGGTGCGCACA
GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCGAGAGGTTG
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTATTGGCCAGTTTAGCCAATCCAAC TGACCTAGTGAAGGTT CAGATGCAAAT
GGAAGGAAAAGGAAACTGGAAGGAAAACCATTGCGATTCTGTGGTACATCATGCATTG
CAAAATCTAGCTGAAGGAGGAATACGAGGGCTTGGCAGGCTGGTACCAATATAACAA
AGAGCAGCACTGGTGAATATGGGAGATTAAACCACTTATGATA CAGTGAAACACTACTGGT
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTATCAAGTTATGTTCTGGAC
TGGTAGCTCTATTCTGGAACACCAGCGATGTCATCAAAGCAGAATAATGAATCAACCA
CGAGATAAACAAAGGAAGGGACTTTGTATAAATCATCGACTGACTGCTGATT CAGGCTGT
TCAAGGTGAAGGATT CATGAGTCTATATAAGGCTTTACCATCTGGCTGAGAATGACCC
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTTTAA

FIGURE 236

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLCVVFGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMOMEGRKRKLEGKPLRFRGVHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRTWPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTGCAGCGC
GCCTGAAGTCGGCGTGGCGTTGAGGAAGCTGGATACAGCATTAAATGAAAAATTATGC
TTAAGAAGTAAAAATGGCAGGCTTCAGATAATTCGTTGGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAAGAAATGCTGTGGCATCTGTTGCGCAGGTATATTGTTTTACAGGC
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAACGCCAGAACAGTTGAACCAGCCTT
TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT
TTCATTGGTTCATGTTGATGTTGGTCACTTATTGCTTCATGTGGATTCTTTGGTGC
ATATGTTACCCAAAATCTGATGTTATCCGGGACTAGCTGTGTTTTCAAAATGCACTTA
TATTTTTAGCACTCTGATCACAAATTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
TTCTTAAGTCACATTTCTTTGTTATATTCTGTTAGATAGGTTTTATCTCTCAGT
ACACATTGCCAAATGGAGTAGATTGATCACATTAAATGTTGTTCTTACATTTATGTT
TGAGTTTGAAATAGTTATGAAATTCTTATTTTCATTGCATAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTATTCTGAGATTAGAA
CTTGATCTACTCCCTGAGCCAGGGTACATCATCTGTCATTTAGAAGTAACCACCTTGT
CTCTGGCTGGCACGGTGGCTATGCCTGTAATCCCAGCACTTGGGAGGCCGAGCGGG
CCGATTGCTTGAGGTCAAGTGTGAGACCAGCCTGGCAACATGGCGAAACCCCATCTACT
AAAAATACAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGAGGC
TGAGGCAGGAGAATCGCTGAACCCGGGGGCAGAGGTTGCAGTGAGCTGAGTTGCCAC
TGCACCTAGCCTGGGGAGAAAGTGAACACTCCCTCTCAAAAAAAAGACCACTCTCAGTATC
TCTGATTTCTGAAGATGTACAAAAAAATAGCTTCATATCTGGAATGAGCACTGAGCCA
TAAAAGGTTTCAGCAAGTTGTAATTATTTGGCCTAAAATGAGGTTTTGGTAAAGA
AAAAATATTGTTCTTATGTATTGAAGAAGTGTACTTTATATAATGATTTTAAATGCC
AAAGGACTAGTTGAAAGCTTCTTTAAAAGAATTCCCTCTAATATGACTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGCAGGAGCAGCTGGCCA
 CTGGCGGCCGCAACACTCCGTCTCACCCCTGGGCCACTGCATCTAGAGGAGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAAGCTGGCCCAGGGTGGT
 GGTCACTGGGTCAAGGACCTACGGCACCTGCTGGACCACCTGCCTCTCCATGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTGGTGGAGCTGACCCCAAGCCACCCCTCACCTGGACAG
GATGAGAGTGTCAAGGTGTGCTCGCCTGGCCCTCATCTTGCCATAGTCACGACATGGA
 TGTTTATTCAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACTAACCTTGCGTTAAATCTGCAGTGGGCCAACGTCTGGCCCTACTATGT
 GCTTGAAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGCAGAGGCCTAACATC
 GCCCTGGTGAATGGAACCACGGAGCTGTGCTGGACAGAAGGCATTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGTGCACTGGTGCTGGTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTCTGACTTG
 GGGAGTTCCCTACGCAAAACAACGGCTCCGGGACAGCTGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAGCCCCTTGAGCAGTTCTAAAGAACAGCCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGGAGATGGAGGGCTGCATGCCCGAAGCCATTTCTAGGGTGGC
 TGTGGCTTCCTCAGCCAGGGCCTGAAGAACGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGTGCTGCGTGGAGGTGCTGCAGGTCTGCACGC
 TGTGTCGCCCTCTCCTCGGAAACAGAACCCCTCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGCTTCTGGAACCAGCTGTGAGGAGAATGGGTGCTTCGTCAAGGG
 ACTGCTGACGGCTGGCCTGAGGAAGGACAAACTGCCAGACTTGAGCCAAATTAAATTAA
 TTTTGCTGGTTTGAAAAA

FIGURE 240

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLLLALIFAIVTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPKPF
```

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCCTGGGAT
 CCAGAAACCCATGATACCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA
 GCAAGAGAACGAGAGATAAATACACTCACGCCAGGAGCTCGCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCAGTCCC
 CTGCACCCCTCCTGGGACACT**ATGT**TGTTCTCCGCCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCCCTGAGTGTGAAACAATGCCAGTCGCCATCGATATTAGACAGACAGTGT
 GACATTTGACCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
 CTTTGGACCTGCACAACAATGCCACACAGTGCAACTCTCTGCCCTCTACCCGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
 CCCAGGGGGTCAGAACACCCAGATCAACAGTGAAGCCACATTGCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT
 GTCTGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCAAGTCAGGCATAAAGATCAGAACACTCAGTGCTCCCTCAACCTAACAGAG
 AGCTGCTCCCCAACAGCTGGGCAGTACTTCCGCTACAATGGCTCGTCACAACCTCCCCCT
 TGCTACCAAGAGTGTGCTCTGGACAGTTTTATAGAAGGTCCCAGATTCAATGGAACAGCT
 GGAAAAGCTTCAGGGACATTGTTCTCCACAGAACAGGAGCCCTCAAGCTCTGGTACAGA
 ACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGTCTTCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTGGTTGGCTGTCTG
 CCTTCTCCTGGCTGTTATTCATTGCTAGAAAGATTGGAAGAACAGGCTGGAAAACCGAA
 AGAGTGTGGTCTCACCTCAGCACAAGCCACGACTGAGGCA**TAA**ATTCTCTCAGATACCA
 TGGATGTGGATGACTCCCTCATGCCTATCAGGAAGCCTCTAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTCCCTGGACATCTTAGAGAG
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACCTGCAGAGCCTTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTGTTAGTTGCAGGG
 GAAGTTGGATATACCCAAAGTCCTCTACCCCTCACTTTATGCCCTTCCCTAGATA
 TACTGCGGGATCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTGATCAATA
 TATTGGAAATTAAAGTTCTGACTTT

FIGURE 242

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IAARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
LPQIFTSLIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGT PAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16



FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGATTGATGCAGCCTGCGCGGCCTCGGAGCGCGGCC
GAGCCAGACGCTGACCACGTTCCCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCG
GCAGCCGGGAGCC**ATG**CGACCCCCAGGGCCCCGCCCTCCCGCAGCGGCTCCGCGGCCCTCC
TGCTGCTCCTGCTGCTGCAGCTGCCCGCCGTCAGCGCCTCTGAGATCCCCAAGGGGAAG
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
GCCAGCAGGAGTGCCTGGTCAGACGGAGCCCTGGGCCAATGTTATTCCGGGTACACCTG
GGATCCCAGGTGGGATGGATTCAAAGGAGAAAAGGGGAATGTCAGGGAAAGCTTGAG
GAGTCCTGGACACCCAACACTACAAGCAGTGGTCATGGAGTTCAATTGAAATTATGGCATAGATCT
TGGAAAATTGCGGAGTGTACATTACAAAGATGCGTTCAAATAGTGCTCTAACAGAGTTTGT
TCAGTGGCTCACTTCGGCTAAATGCAGAAATGCATGCTGCAGCGTTGGTATTCACATTC
AATGGAGCTGAATGTTCAAGGACCTCTTCCCATTGAAGCTATAATTATGGACCAAGGAAG
CCCTGAAATGAATTCAACAATTAATTACATCGCACCTCTGTGGAAAGGACTTGTGAAG
GAATTGGTGTGGATTAGTGGATGTTGCTATCTGGTTGGCACTGTTAGATTACCCAAAA
GGAGATGCTCTACTGGATGGAATTCAAGTTCTCGCATCATTATTGAAGAACTACCCAAA**TA**
AATGCTTAATTTCAATTGCTACCTCTTTTATTATGCCTTGAATGGTCACCTAAAT
GACATTAAATAAGTTATGTATAACATCTGAATGAAAAGCAAAGCTAAATATGTTACAGA
CCAAAGTGTGATTCACACTGTTAAATCTAGCATTATTGCTCAATCAAAGT
GGTTCAATATTTTTAGTTGGTTAGAATACTTCTCATAGTCACATTCTCAACCTA
TAATTGGAATATTGTTGTGGCTTTGTTCTTAGTATAGCATTAAAAAAATA
TAAAAGCTACCAATCTTGTACAATTGTAATGTTAAGAATTAAAAATATCTGTTAAAT
AAAAATTATTCCAACA

FIGURE 246

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pi: 8.43, NX(S/T): 1
MRPQGPAAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN
STINIHRRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217